GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: January 31, 2001, 13:00:02 ; Search time 123.13 Seconds
(without alignments)
6834.114 Million cell updates/sec

Title: US-09-544-776-1
Perfect score: 2240
Sequence: 1 cgtcaccacagtaggtccct.....taaaaaaaaaaaaaaaaaa 2240

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 480022 seqs, 187831343 residues

Word size : 0

Total number of hits satisfying chosen parameters: 960044

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_36:*
1: /SIDS6/gcgdata/geneseq/geneseqn/NA1980.DAT:*
2: /SIDS6/gcgdata/geneseq/geneseqn/NA1981.DAT:*
3: /SIDS6/gcgdata/geneseq/geneseqn/NA1982.DAT:*
4: /SIDS6/gcgdata/geneseq/geneseqn/NA1983.DAT:*
5: /SIDS6/gcgdata/geneseq/geneseqn/NA1984.DAT:*
6: /SIDS6/gcgdata/geneseq/geneseqn/NA1985.DAT:*
7: /SIDS6/gcgdata/geneseq/geneseqn/NA1986.DAT:*
8: /SIDS6/gcgdata/geneseq/geneseqn/NA1987.DAT:*
9: /SIDS6/gcgdata/geneseq/geneseqn/NA1988.DAT:*
10: /SIDS6/gcgdata/geneseq/geneseqn/NA1989.DAT:*
11: /SIDS6/gcgdata/geneseq/geneseqn/NA1990.DAT:*
12: /SIDS6/gcgdata/geneseq/geneseqn/NA1991.DAT:*
13: /SIDS6/gcgdata/geneseq/geneseqn/NA1992.DAT:*
14: /SIDS6/gcgdata/geneseq/geneseqn/NA1993.DAT:*
15: /SIDS6/gcgdata/geneseq/geneseqn/NA1994.DAT:*
16: /SIDS6/gcgdata/geneseq/geneseqn/NA1995.DAT:*
17: /SIDS6/gcgdata/geneseq/geneseqn/NA1996.DAT:*
18: /SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:*
19: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:*
20: /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:*
21: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1558	69.6	1610	21	Z36230	cDNA encoding a bo
2	1122	50.1	1122	21	Z56888	Human MAGI polypep
3	924	41.2	1213	20	X04379	Human secreted pro
4	923	41.2	4093	21	A23454	cDNA encoding huma
5	766	34.2	991	20	X97587	Extended human sec
6	698	31.2	2386	19	V30920	Human secreted pro
7	650	29.0	799	19	V23695	Human NSPLP protei
8	556	24.8	3579	21	Z56886	Human MAGI polypep
9	396	17.7	423	20	V87609	EST clone DY543.
10	241	10.8	404	20	X41193	Human secreted pro
11	214	9.6	301	21	A06512	Human immunogenic
12	171	7.6	439	16	T20045	Human gene signatu
13	95	4.2	211	20	X23499	Human neutrophil c
14	71	3.2	412	20	Z09075	Differentiation In
15	71	3.2	412	21	Z46327	Human differentiat
16	54	2.4	261	19	V23697	Human NSPLP protei
17	31	1.4	444	19	V07231	Human calcitonin r
18	31	1.4	2603	19	V07219	Human calcitonin r
19	28	1.2	2643	14	Q39212	CENP-B cDNA. Homo
20	27	1.2	443	20	Z09056	Differentiation In
21	27	1.2	443	21	Z46308	Human differentiat
22	27	1.2	2518	20	V71745	Human V3 loop HIV
23	26	1.2	2097	19	V26543	Human retinitis pi
24	26	1.2	2115	18	T96642	Human TULP1 cDNA.
25	26	1.2	2223	17	T18679	Human lastin cDNA
26	26	1.2	2358	11	Q07000	Coding part of vec
27	26	1.2	2440	11	Q06469	Sequence encoding
28	26	1.2	3086	11	Q06470	Sequence encoding
29	25	1.1	479	21	D00302	Arabidopsis SERK i
30	25	1.1	1756	21	A12631	cDNA encoding the
31	25	1.1	2932	20	Z11897	Human potassium ch
32	25	1.1	10942	20	V71742	Human V3 loop HIV
33	24	1.1	997	20	Z41269	Human normal ovari
34	24	1.1	1361	20	Z20027	Mouse rad17 cell c
35	24	1.1	1809	20	V99333	Glial cell line-de
36	24	1.1	1878	20	V99334	Glial cell line-de
37	24	1.1	1889	19	V00249	Mouse Ret ligand r
38	24	1.1	1935	21	Z29100	Murine GFRalpha3 c
39	24	1.1	2251	14	Q38723	AII/AVPv2 receptor
40	24	1.1	2424	19	V59725	Human secreted pro
41	24	1.1	2482	20	X90720	Human nn320_2 secr
42	24	1.1	3704	19	V54590	Human secretory pr
43	24	1.1	3704	20	Z25610	Human secreted pro
44	24	1.1	4312	20	Z11738	Human transport-as
45	23	1.0	155	21	Z86979	Retinoblastoma bin

ALIGNMENTS

RESULT 1
Z36230
ID Z36230 standard; cDNA; 1610 BP.
XX
AC Z36230;
XX
DT 22-FEB-2000 (first entry)
XX
DE cDNA encoding a bone marrow secreted protein designated BMS112.
XX
KW Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW erythroid progenitor cell; colony stimulating factor; granulocyte;
KW monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW platelet disorder; thrombocytopenia; hematopoeitic stem cell;
KW stem cell disorder; aplastic anaemia; bone differentiation;
KW paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW bone fracture; cartilage damage; artificial joint; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 132..1253
FT /*tag= a
FT /product= "bone marrow secreted protein"
FT polyA_signal 1516..1521
FT /*tag= b
XX
PN WO9933979-A2.
XX
PD 08-JUL-1999.
XX
PF 18-DEC-1998; 98WO-US27008.

XX
PR 30-DEC-1997; 97US-0068958.
PR 24-SEP-1998; 98US-0101603.
PR 30-SEP-1998; 98US-0102540.
XX
PA (CHIR) CHIRON CORP.
XX
PI Lin H, Cao L;
XX
DR WPI; 2000-038344/03.
DR P-PSDB; Y53624.
XX
PT New isolated human polynucleotide and secreted proteins can induce
PT production of other cytokines in certain cell populations -
XX
PS Claim 11; Page 72-74; 120pp; English.
XX
CC Z36228-49 encode bone marrow secreted proteins of human bone marrow
CC stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC cell differentiation activity (either inducing or inhibiting). They can
CC be used to support colony forming cells or factor-dependent cell lines,
CC to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC deficiencies. In addition, they may be used to support the growth and
CC proliferation of erythroid progenitor cells, and to treat various
CC anaemias. They can have colony stimulating factor (CSF) activity and can
CC be used to support the growth and proliferation of myeloid cells such as
CC granulocytes, monocytes or macrophages, to prevent or treat
CC myelo-suppression, to support the growth and proliferation of
CC megakaryocytes and platelets, thereby allowing prevention or treatment
CC of platelet disorders such as thrombocytopenia, to support the growth
CC and proliferation of hematopoeitic stem cells, either in place of or in
CC conjunction with platelet transfusions, to treat stem cell disorders,
CC such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC repopulate the stem cell compartment after irradiation or chemotherapy.
CC They can be used for growth or differentiation of bone, cartilage,
CC tendon, ligament, or nerve tissue, as well as for wound healing and
CC tissue repair and replacement, and in the treatment of burns, incisions
CC and ulcers, to induce cartilage and/or bone growth in circumstances where
CC bone is not normally formed and thus have an application in healing bone
CC fractures and cartilage damage or defects, prophylactic use in fracture
CC reduction and also in the improved fixation of artificial joints.
XX
SQ Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 other;

Query Match 69.6%; Score 1558; DB 21; Length 1610;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      7 cacagtaggtccctcggctcagtcggcccagcccctctcagtcctccccaaccccacaa 66
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 cacagtaggtccctcggctcagtcggcccagcccctctcagtcctccccaaccccacaa 60

Qy     67 ccgcccgcggctctgagacgcggccccggcggcggcggcagcagctgcagcatcatctcc 126
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ccgcccgcggctctgagacgcggccccggcggcggcggcagcagctgcagcatcatctcc 120

Qy    127 accctccagccatggaagacctggaccagtctcctctggtctcgtcctcggacagcccac 186
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 accctccagccatggaagacctggaccagtctcctctggtctcgtcctcggacagcccac 180

Qy    187 cccggccgcagcccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaag 246
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 cccggccgcagcccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaag 240

Qy    247 aagaggaggaggaagaggaggacgaggacgaagacctggaggagctggaggtgctggaga 306
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 aagaggaggaggaagaggaggacgaggacgaagacctggaggagctggaggtgctggaga 300

Qy    307 ggaagcccgccgccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgc 366
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ggaagcccgccgccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgc 360

Qy    367 ccctgatggacttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccg 426
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ccctgatggacttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccg 420

Qy    427 ctccccccgtcgccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccg 486
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 ctccccccgtcgccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccg 480

Qy    487 tgcccgcgccatccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacg 546
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 tgcccgcgccatccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacg 540

Qy    547 acgagcctccggcccggcctcccctcctcccccggccagcgtgagccccccaggcagagc 606
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 acgagcctccggcccggcctcccctcctcccccggccagcgtgagccccccaggcagagc 600

Qy    607 ccgtgtggaccccgccagccccggctcccgccgcgcccccctccaccccggccgcgccca 666
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 ccgtgtggaccccgccagccccggctcccgccgcgcccccctccaccccggccgcgccca 660

Qy    667 agcgcaggggctcctcgggctcagtggttgttgacctcctgtactggagagacattaaga 726
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 agcgcaggggctcctcgggctcagtggttgttgacctcctgtactggagagacattaaga 720

Qy    727 agactggagtggtgtttggtgccagcctattcctgctgctttcattgacagtattcagca 786
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 agactggagtggtgtttggtgccagcctattcctgctgctttcattgacagtattcagca 780

Qy    787 ttgtgagcgtaacagcctacattgccttggccctgctctctgtgaccatcagctttagga 846
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 ttgtgagcgtaacagcctacattgccttggccctgctctctgtgaccatcagctttagga 840

Qy    847 tatacaagggtgtgatccaagctatccagaaatcagatgaaggccacccattcagggcat 906
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 tatacaagggtgtgatccaagctatccagaaatcagatgaaggccacccattcagggcat 900

Qy    907 atctggaatctgaagttgctatatctgaggagttggttcagaagtacagtaattctgctc 966
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 atctggaatctgaagttgctatatctgaggagttggttcagaagtacagtaattctgctc 960

Qy    967 ttggtcatgtgaactgcacgataaaggaactcaggcgcctcttcttagttgatgatttag 1026
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 ttggtcatgtcaactgcacgataaaggaactcaggcgcctcttcttagttgatgatttag 1020

Qy   1027 ttgattctctgaagtttgcagtgttgatgtgggtatttacctatgttggtgccttgttta 1086
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ttgattctctgaagtttgcagtgttgatgtgggtatttacctatgttggtgccttgttta 1080

Qy   1087 atggtctgacactactgattttggctctcatttcactcttcagtgttcctgttatttatg 1146
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 atggtctgacactactgattttggctctcatttcactcttcagtgttcctgttatttatg 1140

Qy   1147 aacggcatcaggcacagatagatcattatctaggacttgcaaataagaatgttaaagatg 1206
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 aacggcatcaggcacagatagatcattatctaggacttgcaaataagaatgttaaagatg 1200

Qy   1207 ctatggctaaaatccaagcaaaaatccctggattgaagcgcaaagctgaatgaaaacgcc 1266
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 ctatggctaaaatccaagcaaaaatccctggattgaagcgcaaagctgaatgaaaacgcc 1260

Qy   1267 caaaataattagtaggagttcatctttaaaggggatattcatttgattatacgggggagg 1326
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1261 caaaataattagtaggagttcatctttaaaggggatattcatttgattatacgggggagg 1320

Qy   1327 gtcagggaagaacgaaccttgacgttgcagtgcagtttcacagatcgttgttagatcttt 1386
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 gtcagggaagaacgaaccttgacgttgcagtgcagtttcacagatcgttgttagatcttt 1380

Qy   1387 atttttagccatgcactgttgtgaggaaaaattacctgtcttgactgccatgtgttcatc 1446
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 atttttagccatgcactgttgtgaggaaaaattacctgtcttgactgccatgtgttcatc 1440

Qy   1447 atcttaagtattgtaagctgctatgtatggatttaaaccgtaatcatatcttttttcctat 1506
```

```
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 atcttaagtattgtaagctgctatgtatggatttaaaccgtaatcatatctttttcctat 1500

Qy    1507 ctgaggcactggtggaataaaaaacctgtatattttacttttgttgcagatagtcttgccg 1566
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 ctgaggcactggtggaataaaaaacctgtatattttacttttgttgcagatagtcttgccg 1560

Qy    1567 catcttggcaagttgcagagatggtggagctagaaaaaaaaaaaaaaaa 1615
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 catcttggcaagttgcagagatggtggagctagaaaaaaaaaaaaaaaa 1609


RESULT  2
Z56888
ID   Z56888 standard; DNA; 1122 BP.
XX
AC   Z56888;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human MAGI polypeptide variant encoding DNA.
XX
KW   MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW   spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW   psychiatric disorder; developmental disorder; inflammatory disorder;
KW   stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1122
FT                   /*tag=  a
FT                   /product= "MAGI polypeptide"
XX
PN   WO200005364-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;   99WO-GB02360.
XX
PR   22-JUL-1998;   98GB-0016024.
PR   19-JUL-1999;   99GB-0016898.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D,  Prinjha RK;
XX
DR   WPI; 2000-182693/16.
DR   P-PSDB; Y56969.
XX
PT   Novel polypeptides related to neuroendocrine-specific proteins and
PT   polynucleotides useful for diagnosis of various diseases and for
PT   treatment of cancer and neurological disorders -
XX
PS   Claim 5; Page 21-22; 35pp; English.
XX
CC   The invention relates to human MAGI protein, which is similar to
CC   neuroendocrine-specific protein. The MAGI protein can be expressed by
CC   standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC   and antibodies are useful for treating diseases, including neuropathies,
CC   spinal injury, neuronal degeneration, neuromuscular disorders,
CC   psychiatric disorders and developmental disorders, cancer, stroke and
CC   inflammatory disorders. The polynucleoitde is also useful for chromosome
CC   localization and for tissue expression studies. The present sequence
CC   represents a DNA encoding the human MAGI protein variant.
XX
SQ   Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 other;

  Query Match           50.1%;  Score 1122;  DB 21;  Length 1122;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1122;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 atggaagacctggaccagtctcctctggtctcgtcctcggacagcccaccccggccgcag 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atggaagacctggaccagtctcctctggtctcgtcctcggacagcccaccccggccgcag 60

Qy     198 cccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaagaagaggaggag 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 cccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaagaagaggaggag 120

Qy     258 gaagaggaggacgaggacgaagacctggaggagctggaggtgctggagaggaagcccgcc 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 gaagaggaggacgaggacgaagacctggaggagctggaggtgctggagaggaagcccgcc 180

Qy     318 gccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgcccctgatggac 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 gccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgcccctgatggac 240

Qy     378 ttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccgctcccccgtc 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccgctcccccgtc 300

Qy     438 gccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccgtgcccgcgcca 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 gccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccgtgcccgcgcca 360

Qy     498 tccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacgacgagcctccg 557
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 tccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacgacgagcctccg 420

Qy     558 gcccggcctccccctcctccccccggccagcgtgagcccccaggcagagcccgtgtggacc 617
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 gcccggcctccccctcctccccccggccagcgtgagcccccaggcagagcccgtgtggacc 480

Qy     618 ccgccagccccggctcccgccgcgccccccctccaccccggccgcgcgcccaagcgcaggggc 677
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ccgccagccccggctcccgccgcgccccccctccaccccggccgcgcgcccaagcgcaggggc 540

Qy     678 tcctcgggctcagtggttgttgacctcctgtactggagagacattaagaagactggagtg 737
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 tcctcgggctcagtggttgttgacctcctgtactggagagacattaagaagactggagtg 600

Qy     738 gtgtttggtgccagcctattcctgctgctttcattgacagtattcagcattgtgagcgta 797
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 gtgtttggtgccagcctattcctgctgctttcattgacagtattcagcattgtgagcgta 660

Qy     798 acagcctacattgccttggccctgctctctgtgaccatcagctttaggatatacaagggt 857
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 acagcctacattgccttggccctgctctctgtgaccatcagctttaggatatacaagggt 720

Qy     858 gtgatccaagctatccagaaatcagatgaaggccacccattcagggcatatctggaatct 917
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 gtgatccaagctatccagaaatcagatgaaggccacccattcagggcatatctggaatct 780

Qy     918 gaagttgctatatctgaggagttggttcagaagtacagtaattctgctcttggtcatgtg 977
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 gaagttgctatatctgaggagttggttcagaagtacagtaattctgctcttggtcatgtg 840

Qy     978 aactgcacgataaaggaactcaggcgcctcttcttagttgatgatttagttgattctctg 1037
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 aactgcacgataaaggaactcaggcgcctcttcttagttgatgatttagttgattctctg 900

Qy    1038 aagtttgcagtgttgatgtgggtatttacctatgttggtgccttgtttaatggtctgaca 1097
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 aagtttgcagtgttgatgtgggtatttacctatgttggtgccttgtttaatggtctgaca 960

Qy    1098 ctactgattttggctctcatttcactcttcagtgttcctgttatttatgaacggcatcag 1157
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 ctactgattttggctctcatttcactcttcagtgttcctgttatttatgaacggcatcag 1020

Qy    1158 gcacagatagatcattatctaggacttgcaaataagaatgttaaagatgctatggctaaa 1217
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 gcacagatagatcattatctaggacttgcaaataagaatgttaaagatgctatggctaaa 1080

Qy    1218 atccaagcaaaaatccctggattgaagcgcaaagctgaatga 1259
```

```
                                          ||||||||||||||||||||||||||||||||||||||||
Db   1081 atccaagcaaaaatccctggattgaagcgcaaagctgaatga 1122


RESULT   3
X04379
ID   X04379 standard; DNA; 1213 BP.
XX
AC   X04379;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human secreted protein gene 69 clone HAGFT48.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9856804-A1.
XX
PD   17-DEC-1998.
XX
PF   11-JUN-1998;   98WO-US12125.
XX
PR   02-OCT-1997;   97US-0061060.
PR   13-JUN-1997;   97US-0049547.
PR   13-JUN-1997;   97US-0049548.
PR   13-JUN-1997;   97US-0049549.
PR   13-JUN-1997;   97US-0049550.
PR   13-JUN-1997;   97US-0049606.
PR   13-JUN-1997;   97US-0049607.
PR   13-JUN-1997;   97US-0049608.
PR   13-JUN-1997;   97US-0049609.
PR   13-JUN-1997;   97US-0049610.
PR   13-JUN-1997;   97US-0049611.
PR   13-JUN-1997;   97US-0050566.
PR   13-JUN-1997;   97US-0050901.
PR   13-JUN-1997;   97US-0052989.
PR   08-JUL-1997;   97US-0051919.
PR   18-AUG-1997;   97US-0055984.
PR   12-SEP-1997;   97US-0058665.
PR   12-SEP-1997;   97US-0058668.
PR   12-SEP-1997;   97US-0058669.
PR   12-SEP-1997;   97US-0058750.
PR   12-SEP-1997;   97US-0058971.
PR   12-SEP-1997;   97US-0058972.
PR   12-SEP-1997;   97US-0058975.
PR   02-OCT-1997;   97US-0060834.
PR   02-OCT-1997;   97US-0060841.
PR   02-OCT-1997;   97US-0060844.
PR   02-OCT-1997;   97US-0060865.
PR   02-OCT-1997;   97US-0061059.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Brewer LA,  Ebner R,  Ferrie AM,  Feng P,  Greene JM,  Lafleur DW;
PI   Moore PA,  Ni J,  Olsen HS,  Rosen CA,  Ruben SM,  Shi Y,  Young P;
PI   Yu GL;
XX
DR   WPI; 1999-080881/07.
DR   P-PSDB; W78194.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
XX
PS   Claim 1; Page 235-236; 380pp; English.
XX
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein.  The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line.  The gene can be used to generate fusion
CC   proteins by linking to the gene to a human immunoglobulin Fc portion
CC   (e.g. X04302) for increasing the stability of the fused protein as
CC   compared to the human protein only.
CC   The invention relates to 86 novel genes and their fragments (nucleic acid
CC   sequences: X04311-X04410; amino acid sequences W78126-W78225) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 86 polynucleotides, based on
CC   which tissues they are most highly expressed in (see X04311 for described
CC   uses).
XX
SQ   Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 4 other;


  Query Match             41.2%;  Score 924;  DB 20;  Length 1213;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  924;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     692 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 306

Qy     752 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 366

Qy     812 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     367 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 426

Qy     872 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 931
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     427 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 486

Qy     932 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 991
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     487 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 546

Qy     992 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 1051
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     547 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 606

Qy    1052 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 1111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     607 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 666

Qy'   1112 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 1171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     667 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 726

Qy    1172 ttatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 1231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     727 ttatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 786

Qy    1232 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 1291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     787 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 846

Qy    1292 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgt 1351
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     847 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgt 906

Qy    1352 tgcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgag 1411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     907 tgcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgag 966
```

```
Qy   1412 gaaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatg 1471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    967 gaaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatg 1026

Qy   1472 tatggatttaaaccgtaatcatatctttttcctatctgaggcactggtggaataaaaaac 1531
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1027 tatggatttaaaccgtaatcatatctttttcctatctgaggcactggtggaataaaaaac 1086

Qy   1532 ctgtatattttacttttgttgcagatagtcttgccgcatcttggcaagttgcagagatggt 1591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1087 ctgtatattttacttttgttgcagatagtcttgccgcatcttggcaagttgcagagatggt 1146

Qy   1592 ggagctagaaaaaaaaaaaaaaaa 1615
          ||||||||||||||||||||||||
Db   1147 ggagctagaaaaaaaaaaaaaaaa 1170


RESULT   4
A23454
ID   A23454 standard; cDNA; 4093 BP.
XX
AC   A23454;
XX
DT   19-JUN-2000  (first entry)
XX
DE   cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW   Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW   blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW   infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW   neurodegenerative disease; asthma; contraceptive; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1048..3729
FT                   /*tag= a
FT                   /product= "Human secreted protein vb22_1"
FT   CDS             152..1006
FT                   /*tag= b
FT                   /product= "Clone vb22_1 ORF2"
XX
PN   WO200011015-A1.
XX
PD   02-MAR-2000.
XX
PF   24-AUG-1999;   99WO-US19351.
XX
PR   24-AUG-1998;   98US-0097638.
PR   24-AUG-1998;   98US-0097659.
PR   09-SEP-1998;   98US-0099618.
PR   28-SEP-1998;   98US-0102092.
PR   25-NOV-1998;   98US-0109978.
PR   23-DEC-1998;   98US-0113645.
PR   23-DEC-1998;   98US-0113646.
PR   23-AUG-1999;   99US-0379246.
XX
PA   (ALPH-) ALPHAGENE INC.
XX
PI   Valenzuela D,  Yuan O,  Hoffman H,  Hall J,  Rapiejko P;
XX
DR   WPI; 2000-224657/19.
DR   P-PSDB; Y95012, Y95030.
XX
PT   New secreted or transmembrane proteins and polynucleotides encoding
PT   them, useful for treating neurodegenerative disorders, autoimmune
PT   diseases and cancer -
XX
PS   Claim 72; Page 321-322; 357pp; English.
XX
CC   The invention relates to 40 human secreted proteins (Y94981-Y95020),
CC   and cDNA sequences encoding them (A23423-A23462). The secreted proteins
CC   of the invention include those that are thought to be only partially
CC   secreted, i.e., transmembrane proteins. The proteins of the invention may
CC   exhibit one or more activities selected from the following: cytokine
CC   activity; cell proliferation; differentiation; immune modulation;
CC   haematopoiesis regulation; tissue growth activity; activin/inhibin
CC   activity; chemotactic/chemokinetic activity; haemostatic and
CC   thrombolytic activity; anti-inflammatory activity; and tumour inhibition
CC   activity. The proteins may be administered to patients as vaccines, and
CC   the nucleotides may be used as part of a gene therapy regime. Diseases or
CC   conditions that may be treated using the proteins or nucleotides of the
CC   invention include autoimmune diseases; genetic disorders; haemophilia;
CC   cardiovascular diseases; cancer; bacterial, fungal and viral infections,
CC   especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary
CC   inflammation; Guillain-Barre syndrome; insulin dependent diabetes
CC   mellitus; and allergic reactions such as asthma and anaemia. They may
CC   also be used for treating wounds, burns, ulcers, osteoporosis,
CC   osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's
CC   disease, Huntington's disease and amyotrophic lateral sclerosis (ALS).
CC   Proteins with activin/inhibin activity may additionally be useful as
CC   contraceptives. Nucleic acid sequences of the invention may be used in
CC   chromosome mapping, and as a source of diagnostic primers and probes.
CC   The present sequence represents cDNA encoding one of the 40 proteins of
CC   the invention.
XX
SQ   Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 other;


  Query Match             41.2%;  Score 923;  DB 21;  Length 4093;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  923;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    693 gttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccagc 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3163 gttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccagc 3222

Qy    753 ctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgcc 812
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3223 ctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgcc 3282

Qy    813 ttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctatc 872
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3283 ttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctatc 3342

Qy    873 cagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatct 932
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3343 cagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatct 3402

Qy    933 gaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaag 992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3403 gaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaag 3462

Qy    993 gaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgttg 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3463 gaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgttg 3522

Qy   1053 atgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggct 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3523 atgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggct 3582

Qy   1113 ctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatcat 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3583 ctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatcat 3642

Qy   1173 tatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaatc 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3643 tatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaatc 3702

Qy   1233 cctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatctt 1292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3703 cctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatctt 3762

Qy   1293 taaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgtt 1352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3763 taaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgtt 3822
```

```
Qy   1353 gcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgagg 1412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3823 gcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgagg 3882

Qy   1413 aaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatgt 1472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3883 aaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatgt 3942

Qy   1473 atggatttaaaccgtaatcatatctttttcctatctgaggcactggtggaataaaaaacc 1532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3943 atggatttaaaccgtaatcatatctttttcctatctgaggcactggtggaataaaaaacc 4002

Qy   1533 tgtatattttactttgttgcagatagtcttgccgcatcttggcaagttgcagagatggtg 1592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   4003 tgtatattttactttgttgcagatagtcttgccgcatcttggcaagttgcagagatggtg 4062

Qy   1593 gagctagaaaaaaaaaaaaaaaa 1615
          ||||||||||||||||||||||
Db   4063 gagctagaaaaaaaaaaaaaaaa 4085
```

```
RESULT   5
X97587
ID   X97587 standard; DNA; 991 BP.
XX
AC   X97587;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Extended human secreted protein coding sequence, SEQ ID NO. 51.
XX
KW   Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW   cellular differentiation; immune system regulator; anti-inflammatory;
KW   haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW   reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW   genetic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9931236-A2.
XX
PD   24-JUN-1999.
XX
PF   17-DEC-1998;   98WO-IB02122.
XX
PR   10-AUG-1998;   98US-0096116.
PR   17-DEC-1997;   97US-0069957.
PR   09-FEB-1998;   98US-0074121.
PR   13-APR-1998;   98US-0081563.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Duclert A,  Dumas Milne Edwards J;
XX
DR   WPI; 1999-385906/32.
DR   P-PSDB; Y35903.
XX
PT   New isolated human secreted proteins
XX
PS   Claim 1; Page 185-186; 516pp; English.
XX
CC   This sequence represents an extended human secreted protein coding
CC   sequence of the invention. The secreted proteins can be used in treating
CC   or controlling a variety of human conditions. The secreted proteins may
CC   act as cytokines or may affect cellular proliferation or differentiation
CC   or may act as immune system regulators, haematopoiesis regulators, tissue
CC   growth regulators, regulators of reproductive hormones or cell movement
CC   or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC   tumour inhibition activity. The DNAs can be used in forensic procedures
CC   to identify individuals or in diagnostic procedures to identify
CC   individuals having genetic diseases resulting from abnormal expression of
CC   the genes corresponding to the extended cDNAs. They are also useful for
CC   constructing a high resolution map of the human chromosomes. They can
CC   also be used for gene therapy to control or treat genetic diseases.
XX
SQ   Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 other;
```

```
  Query Match             34.2%;  Score 766;  DB 20;  Length 991;
  Best Local Similarity   99.9%;  Pred. No. 1.3e-268;
  Matches  816;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    692 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     67 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 126

Qy    752 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 811
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    127 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 186

Qy    812 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 871
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    187 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 246

Qy    872 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 931
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    247 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 306

Qy    932 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 991
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 366

Qy    992 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 1051
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    367 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 426

Qy   1052 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 1111
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    427 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 486

Qy   1112 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 1171
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    487 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 546

Qy   1172 ttatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 1231
          |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    547 ttatctagtacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 606

Qy   1232 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 1291
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    607 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 666

Qy   1292 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgt 1351
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    667 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacgaaccttgacgt 726

Qy   1352 tgcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgag 1411
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    727 tgcagtgcagtttcacagatcgttgttagatctttatttttagccatgcactgttgtgag 786

Qy   1412 gaaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatg 1471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    787 gaaaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatg 846

Qy   1472 tatggatttaaaccgtaatcatatctttttcctatct 1508
          |||||||||||||||||||||||||||||||||||||
Db    847 tatggatttaaaccgtaatcatatctttttcctatct 883
```

```
RESULT   6
V30920
ID   V30920 standard; cDNA; 2386 BP.
XX
AC   V30920;
XX
```

```
DT   14-SEP-1998  (first entry)
XX
DE   Human secreted protein BG160_1 cDNA.
XX
KW   BG160_1; secreted protein; protein factor; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             102..2030
FT                   /*tag= a
FT   sig_peptide     1863..1899
FT                   /*tag= b
FT                   /note= "putative leader/signal peptide"
FT   mat_peptide     1900..2027
FT                   /*tag= c
XX
PN   WO9817687-A2.
XX
PD   30-APR-1998.
XX
PF   24-OCT-1997;   97WO-US19590.
XX
PR   24-OCT-1997;   97US-0740274.
PR   25-OCT-1996;   96US-0740274.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1998-261426/23.
DR   P-PSDB; W58383.
XX
PT   Nucleic acid encoding secreted protein from human cells - useful,
PT   e.g. as immunomodulator, antitumour agent, promoters of tissue
PT   growth, haemostatic and thrombolytic agents etc.
XX
PS   Claim 20; Page 74-75; 114pp; English.
XX
CC   This cDNA clone, designated BG160_1, codes for a novel human
CC   secreted protein (see W58383). It was isolated from a human adult
CC   brain cDNA library using methods selective for cDNAs that encode
CC   secreted proteins.  The clone is deposited in composite clone
CC   ATCC 98232; an oligonucleotide (see T99725) is designed to isolate
CC   the clone from the composite.  The predicted AT415_4 amino acid
CC   sequence shows homology to neuroendocrine-specific proteins.  Novel
CC   cDNA clones (see V30916-32) coding for human secreted proteins (see
CC   W58580-90) are claimed.  These can be used for recombinant
CC   production of the secreted proteins for analysis, characterisation,
CC   diagnostic or therapeutic use.  They can also be used as tissue or
CC   mol.wt. markers, for chromosome identification, to identify genetic
CC   disorders, to isolate new related DNA, as sources of primers for
CC   PCR, to generate antibodies, and in interaction trap assays.  The
CC   secreted proteins may also have many biological activities, e.g.
CC   cytokine, immunomodulator, haematopoiesis regulating activity,
CC   tissue growth activity, activin or inhibin activity, chemotactic or
CC   chemokinetic activity, haemostatic and thrombolytic activity,
CC   receptor/ligand activity, antiinflammatory, cadherin and tumour
CC   invasion suppressor activity, and tumour inhibition activity.  The
CC   proteins can be expressed in vivo from DNA, introduced in gene
CC   therapy vectors.
XX
SQ   Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;


  Query Match             31.2%;  Score 698;  DB 19;  Length 2386;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-244;
  Matches  698;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     918 gaagttgctatatctgaggagttggttcagaagtacagtaattctgctcttggtcatgtg 977
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1689 gaagttgctatatctgaggagttggttcagaagtacagtaattctgctcttggtcatgtg 1748

Qy     978 aactgcacgataaaggaactcaggcgcctcttcttagttgatgatttagttgattctctg 1037
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1749 aactgcacgataaaggaactcaggcgcctcttcttagttgatgatttagttgattctctg 1808

Qy    1038 aagtttgcagtgttgatgtgggtatttacctatgttggtgccttgtttaatggtctgaca 1097
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1809 aagtttgcagtgttgatgtgggtatttacctatgttggtgccttgtttaatggtctgaca 1868

Qy    1098 ctactgattttggctctcatttcactcttcagtgttcctgttatttatgaacggcatcag 1157
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1869 ctactgattttggctctcatttcactcttcagtgttcctgttatttatgaacggcatcag 1928

Qy    1158 gcacagatagatcattatctaggacttgcaaataagaatgttaaagatgctatggctaaa 1217
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1929 gcacagatagatcattatctaggacttgcaaataagaatgttaaagatgctatggctaaa 1988

Qy    1218 atccaagcaaaaatccctggattgaagcgcaaagctgaatgaaaacgcccaaaataatta 1277
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1989 atccaagcaaaaatccctggattgaagcgcaaagctgaatgaaaacgcccaaaataatta 2048

Qy    1278 gtaggagttcatctttaaaggggatattcatttgattatacgggggagggtcagggaaga 1337
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2049 gtaggagttcatctttaaaggggatattcatttgattatacgggggagggtcagggaaga 2108

Qy    1338 acgaaccttgacgttgcagtgcagtttcacagatcgttgttagatctttatttttagcca 1397
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2109 acgaaccttgacgttgcagtgcagtttcacagatcgttgttagatctttatttttagcca 2168

Qy    1398 tgcactgttgtgaggaaaaattacctgtcttgactgccatgtgttcatcatcttaagtat 1457
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2169 tgcactgttgtgaggaaaaattacctgtcttgactgccatgtgttcatcatcttaagtat 2228

Qy    1458 tgtaagctgctatgtatggatttaaaccgtaatcatatctttttcctatctgaggcactg 1517
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2229 tgtaagctgctatgtatggatttaaaccgtaatcatatctttttcctatctgaggcactg 2288

Qy    1518 gtggaataaaaaacctgtatatttttactttgttgcagatagtcttgccgcatcttggcaa 1577
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2289 gtggaataaaaaacctgtatatttttactttgttgcagatagtcttgccgcatcttggcaa 2348

Qy    1578 gttgcagagatggtggagctagaaaaaaaaaaaaaaaa 1615
          ||||||||||||||||||||||||||||||||||||||
Db    2349 gttgcagagatggtggagctagaaaaaaaaaaaaaaaa 2386


RESULT   7
V23695
ID   V23695 standard; cDNA; 799 BP.
XX
AC   V23695;
XX
DT   24-JUL-1998  (first entry)
XX
DE   Human NSPLP protein A coding sequence.
XX
KW   NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW   neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..674
FT                   /*tag= a
FT                   /product= NSPLPA
XX
PN   WO9806841-A2.
XX
PD   19-FEB-1998.
XX
PF   24-JUL-1997;   97WO-US13469.
XX
PR   12-AUG-1996;   96US-0700607.
```

```
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Bandman O,  Goli SK,  Hillman J;
XX
DR   WPI; 1998-159533/14.
DR   P-PSDB; W53947.
XX
PT   Human neuro-endocrine-specific protein-like proteins - useful for
PT   diagnosis, monitoring and treatment of cancer and neuro-degenerative
PT   disease
XX
PS   Claim 3; Page 38-39; 73pp; English.
XX
CC   This sequence encodes a human neuroendocrine-specific protein-like
CC   protein (NSPLP) of the invention. Recombinant cells transformed with the
CC   DNA are used to express the NSPLP proteins, which are used to treat
CC   cancer and neurodegenerative diseases such as amyotrophic lateral
CC   sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
CC   used to inhibit activity of the NSPLP proteins. Antibodies specific for
CC   NSPLP are used for diagnosis and monitoring treatment of diseases
CC   associated with NSPLP expression, in usual immunoassays, and to isolate
CC   NSPLP from natural sources. The NSPLP proteins, or their fragments can
CC   also be used in drug screening to identify NSPLP antagonists. The nucleic
CC   acid can be used diagnostically and for monitoring treatment (in
CC   hybridisation or amplification assays); to isolate closely related
CC   sequences; in gene therapy for both sense and antisense applications
CC   (including use of ribozymes) and for mapping the natural genomic
CC   sequence.
XX
SQ   Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 2 other;


  Query Match             29.0%;  Score 650;  DB 19;  Length 799;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-226;
  Matches  650;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     692 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     107 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 166

Qy     752 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     167 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 226

Qy     812 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     227 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 286

Qy     872 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 931
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     287 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 346

Qy     932 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 991
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     347 tgaggagttggttcagaagtacagtaattctgctcttggtcatgtgaactgcacgataaa 406

Qy     992 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 1051
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     407 ggaactcaggcgcctcttcttagttgatgatttagttgattctctgaagtttgcagtgtt 466

Qy    1052 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 1111
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     467 gatgtgggtatttacctatgttggtgccttgtttaatggtctgacactactgattttggc 526

Qy    1112 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 1171
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     527 tctcatttcactcttcagtgttcctgttatttatgaacggcatcaggcacagatagatca 586

Qy    1172 ttatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 1231
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     587 ttatctaggacttgcaaataagaatgttaaagatgctatggctaaaatccaagcaaaaat 646

Qy    1232 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 1291
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     647 ccctggattgaagcgcaaagctgaatgaaaacgcccaaaataattagtaggagttcatct 706

Qy    1292 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacga 1341
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db     707 ttaaaggggatattcatttgattatacgggggagggtcagggaagaacga 756


RESULT   8
Z56886
ID   Z56886 standard; DNA; 3579 BP.
XX
AC   Z56886;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human MAGI polypeptide encoding DNA.
XX
KW   MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW   spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW   psychiatric disorder; developmental disorder; inflammatory disorder;
KW   stroke; cytostatic; cerebroprotective; neuroprotective; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3579
FT                   /*tag= a
FT                   /product= "MAGI polypeptide"
XX
PN   WO200005364-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;   99WO-GB02360.
XX
PR   22-JUL-1998;   98GB-0016024.
PR   19-JUL-1999;   99GB-0016898.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D,  Prinjha RK;
XX
DR   WPI; 2000-182693/16.
DR   P-PSDB; Y56967.
XX
PT   Novel polypeptides related to neuroendocrine-specific proteins and
PT   polynucleotides useful for diagnosis of various diseases and for
PT   treatment of cancer and neurological disorders -
XX
PS   Claim 5; Page 19-20; 35pp; English.
XX
CC   The invention relates to human MAGI protein, which is similar to
CC   neuroendocrine-specific protein. The MAGI protein can be expressed by
CC   standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC   and antibodies are useful for treating diseases, including neuropathies,
CC   spinal injury, neuronal degeneration, neuromuscular disorders,
CC   psychiatric disorders and developmental disorders, cancer, stroke and
CC   inflammatory disorders. The polynucleoitde is also useful for chromosome
CC   localization and for tissue expression studies. The present sequence
CC   represents a DNA encoding the human MAGI protein.
XX
SQ   Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;


  Query Match             24.8%;  Score 556;  DB 21;  Length 3579;
  Best Local Similarity   100.0%;  Pred. No. 1e-192;
  Matches  556;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     138 atggaagacctggaccagtctcctctggtctcgtcctcggacagcccaccccggccgcag 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 atggaagacctggaccagtctcctctggtctcgtcctcggacagcccaccccggccgcag 60
```

```
Qy    198 cccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaagaagaggaggag 257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 cccgcgttcaagtaccagttcgtgagggagcccgaggacgaggaggaagaagaggaggag 120

Qy    258 gaagaggaggacgaggacgaagacctggaggagctggaggtgctggagaggaagcccgcc 317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 gaagaggaggacgaggacgaagacctggaggagctggaggtgctggagaggaagcccgcc 180

Qy    318 gccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgcccctgatggac 377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 gccgggctgtccgcggccccagtgcccaccgcccctgccgccggcgcgcccctgatggac 240

Qy    378 ttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccgctccccccgtc 437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 ttcggaaatgacttcgtgccgccggcgccccggggaccccctgccggccgctccccccgtc 300

Qy    438 gccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccgtgcccgcgcca 497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 gccccggagcggcagccgtcttgggacccgagcccggtgtcgtcgaccgtgcccgcgcca 360

Qy    498 tccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacgacgagcctccg 557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 tccccgctgtctgctgccgcagtctcgccctccaagctccctgaggacgacgagcctccg 420

Qy    558 gcccggcctcccccctcctccccccggccagcgtgagcccccaggcagagcccgtgtggacc 617
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 gcccggcctcccccctcctccccccggccagcgtgagcccccaggcagagcccgtgtggacc 480

Qy    618 ccgccagccccggctcccgccgcgccccccctccaccccggccgcgcccaagcgcaggggc 677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 ccgccagccccggctcccgccgcgccccccctccaccccggccgcgcccaagcgcaggggc 540

Qy    678 tcctcgggctcagtgg 693
          ||||||||||||||||
Db    541 tcctcgggctcagtgg 556
```

RESULT 9
V87609
ID V87609 standard; cDNA; 423 BP.
XX
AC V87609;
XX
DT 12-FEB-1999 (first entry)
XX
DE EST clone DY543.
XX
KW Expressed sequence tag; secreted protein; haematopoiesis regulator;
KW tissue growth; activin; inhibin; tumour invasion suppressor; EST; human;
KW chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
KW receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
XX
OS Homo sapiens.
XX
PN WO9845437-A2.
XX
PD 15-OCT-1998.
XX
PF 10-APR-1998; 98WO-US06956.
XX
PR 10-APR-1997; 97US-0837312.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D;
PI Racie LA, Spaulding V, Treacy M;
XX
DR WPI; 1999-070078/06.
XX
PT New polynucleotides encoding human secreted proteins - derived from
PT e.g. human blood, kidney, foetal lung, placenta, testes, brain,
PT ovary, pituitary, retina and colon cDNA libraries
XX
PS Claim 1; Page 120; 641pp; English.
XX
CC The present sequence represents an expressed sequence tag (EST), and is
CC a polynucleotide of the invention. The polynucleotides of the invention
CC are all secreted EST sequences isolated from a variety of human tissue
CC sources. The EST sequences and proteins encoded by them are predicted to
CC have useful biological activities which would make them suitable for
CC treating, preventing or ameliorating medical conditions in humans and
CC animals, although no supporting data is given. Suggested activities
CC include nutritional activity, immune stimulating or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, tumour inhibition
CC activity. The EST sequences are also stated to be useful for gene
CC therapy.
XX
SQ Sequence 423 BP; 135 A; 76 C; 79 G; 133 T; 0 other;

Query Match 17.7%; Score 396; DB 20; Length 423;
Best Local Similarity 100.0%; Pred. No. 1.1e-134;
Matches 396; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1594 agctagaaaaaaaaaaaaaaaaagccctttttcagtttgtgcactgtgtatggtccgtgtag 1653
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 agctagaaaaaaaaaaaaaaaaagccctttttcagtttgtgcactgtgtatggtccgtgtag 80

Qy   1654 attgatgcagattttctgaaatgaaatgtttgtttagacgagatcataccggtaaagcag 1713
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 attgatgcagattttctgaaatgaaatgtttgtttagacgagatcataccggtaaagcag 140

Qy   1714 gaatgacaaagcttgcttttctggtatgttctaggtgtattgtgacttttactgttatat 1773
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 gaatgacaaagcttgcttttctggtatgttctaggtgtattgtgacttttactgttatat 200

Qy   1774 taattgccaatataagtaaatatagattatatatgtatagtgtttcacaaagcttagacc 1833
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 taattgccaatataagtaaatatagattatatatgtatagtgtttcacaaagcttagacc 260

Qy   1834 tttaccttccagccaccccacagtgcttgatatttcagagtcagtcattggttatacatg 1893
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    261 tttaccttccagccaccccacagtgcttgatatttcagagtcagtcattggttatacatg 320

Qy   1894 tgtagttccaaagcacataagctagaagaagaaatatttctaggagcactaccatctgtt 1953
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    321 tgtagttccaaagcacataagctagaagaagaaatatttctaggagcactaccatctgtt 380

Qy   1954 ttcaacatgaaatgccacacacatagaactccaaca 1989
          ||||||||||||||||||||||||||||||||||||
Db    381 ttcaacatgaaatgccacacacatagaactccaaca 416
```

RESULT 10
X41193
ID X41193 standard; cDNA; 404 BP.
XX
AC X41193;
XX
DT 17-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO:137.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens.
XX

```
PN   WO9906548-A2.
XX
PD   11-FEB-1999.
XX
PF   31-JUL-1998;   98WO-IB01222.
XX
PR   01-AUG-1997;   97US-0905135.
XX
PA   (GEST ) GENSET.
XX
PI   Duclert A,  Dumas Milne Edwards J,  Lacroix B;
XX
DR   WPI; 1999-153778/13.
DR   P-PSDB; Y12360.
XX
PT   New nucleic acids encoding human secreted proteins - obtained from
PT   cDNA libraries prepared from e.g. liver, ovary, brain, prostate,
PT   kidney, lung, umbilical cord, placenta and colon tissue
XX
PS   Claim 1; Page 319; 824pp; English.
XX
CC   X41094 to X41347 represent 5' expressed sequence tags (ESTs) for human
CC   secreted proteins, and encode the proteins given in Y12261 to Y12514,
CC   respectively. The proteins given represent the signal peptide and an
CC   N-terminal fragment of a secreted protein. The nucleic acid sequences
CC   can be used for producing secreted human gene products. They can also
CC   be used to develop products for diagnosis and therapy. The proteins
CC   obtained may have cytokine activity, cell proliferation/differentiation
CC   activity, haematopoiesis regulating activity, tissue growth regulating
CC   activity, reproductive hormone regulating activity, chemotactic/
CC   chemokinetic activity, haemostatic and thrombolytic activity, receptor/
CC   ligand activity, anti-inflammatory activity, tumour inhibition activity
CC   or other activities. The products can be used in forensic, gene therapy
CC   and chromosome mapping procedures. The sequences can also be used for
CC   obtaining corresponding promoter sequences. The nucleic acids encoding
CC   the signal peptide can be used for directing extracellular secretion of
CC   a polypeptide or the insertion of a polypeptide into a membrane, or
CC   importing a polypeptide into a cell.
XX
SQ   Sequence 404 BP; 110 A; 75 C; 108 G; 111 T; 0 other;


  Query Match             10.8%;  Score 241;  DB 20;  Length 404;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-78;
  Matches  241;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     692 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 751
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     164 ggttgttgacctcctgtactggagagacattaagaagactggagtggtgtttggtgccag 223

Qy     752 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 811
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     224 cctattcctgctgctttcattgacagtattcagcattgtgagcgtaacagcctacattgc 283

Qy     812 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 871
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     284 cttggccctgctctctgtgaccatcagctttaggatatacaagggtgtgatccaagctat 343

Qy     872 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 931
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     344 ccagaaatcagatgaaggccacccattcagggcatatctggaatctgaagttgctatatc 403

Qy     932 t 932
           |
Db     404 t 404


RESULT  11
A06512
ID   A06512 standard; cDNA; 301 BP.
XX
AC   A06512;
XX
DT   13-JUN-2000  (first entry)
XX
DE   Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:279.
XX
KW   Human; prostate cancer; diagnosis; tumour; gene therapy; detection;
KW   immunogenic; cytostatic; vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200004149-A2.
XX
PD   27-JAN-2000.
XX
PF   14-JUL-1999;   99WO-US15838.
XX
PR   14-JUL-1998;   98US-0115453.
PR   14-JUL-1998;   98US-0116134.
PR   23-SEP-1998;   98US-0159812.
PR   23-SEP-1998;   98US-0159822.
PR   15-JAN-1999;   99US-0232149.
PR   15-JAN-1999;   99US-0232880.
PR   09-APR-1999;   99US-0288946.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Dillon DC,  Harlocker SL,  Yuqiu J,  Xu J,  Mitcham JL;
XX
DR   WPI; 2000-171268/15.
XX
PT   New polypeptide useful for treating and diagnosing prostate cancer
PT   comprises an immunogenic portion of prostate tumor protein -
XX
PS   Claim 1; Page 190; 263pp; English.
XX
CC   The present invention describes isolated polypeptides, comprising an
CC   immunogenic portion of a prostate tumour protein (PTP). The polypeptides
CC   and polynucleotides encoding them have cytostatic activity and can be
CC   used in vaccines and in gene therapy. The polypeptides and
CC   polynucleotides encoding them, antigen presenting cells which express
CC   the polypeptides, antibodies against the polypeptides and vaccines
CC   comprising them can be used for inhibiting the development of prostate
CC   cancer in a patient. The polypeptides can be used to generate antibodies
CC   or anti-idiotypic antibodies for passive immuno therapy. A portion of
CC   the polynucleotides encoding the polypeptides can be used as a probe or
CC   to modulate the expression of the polypeptides. A06241 to A06691 and
CC   Y82000 to Y82020 represent sequences used in the exemplification of the
CC   present invention.
XX
SQ   Sequence 301 BP; 98 A; 57 C; 48 G; 96 T; 2 other;


  Query Match             9.6%;  Score 214;  DB 21;  Length 301;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-69;
  Matches  214;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1707 aaagcaggaatgacaaagcttgcttttctggtatgttctaggtgtattgtgacttttact 1766
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 aaagcaggaatgacaaagcttgcttttctggtatgttctaggtgtattgtgacttttact 60

Qy    1767 gttatattaattgccaatataagtaaatatagattatatatgtatagtgtttcacaaagc 1826
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 gttatattaattgccaatataagtaaatatagattatatatgtatagtgtttcacaaagc 120

Qy    1827 ttagacctttaccttccagccaccccacagtgcttgatatttcagagtcagtcattggtt 1886
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 ttagacctttaccttccagccaccccacagtgcttgatatttcagagtcagtcattggtt 180

Qy    1887 atacatgtgtagttccaaagcacataagctagaa 1920
           ||||||||||||||||||||||||||||||||||
Db     181 atacatgtgtagttccaaagcacataagctagaa 214


RESULT  12
```

```
T20045
ID   T20045 standard; cDNA to mRNA; 439 BP.
XX
AC   T20045;
XX
DT   17-JUL-1996  (first entry)
XX
DE   Human gene signature HUMGS01184.
XX
KW   Gene signature; messenger RNA; mRNA; relative abundance; frequency;
KW   human; cloning; mapping; non-biased library; diagnosis; detection;
KW   cell typing; abnormal cell function; ss.
XX
OS   Homo sapiens.
XX
PN   WO9514772-A1.
XX
PD   01-JUN-1995.
XX
PF   11-NOV-1994;   94WO-JP01916.
XX
PR   12-NOV-1993;   93JP-0355504.
XX
PA   (MATS/) MATSUBARA K.
PA   (OKUB/) OKUBO K.
XX
PI   Matsubara K,  Okubo K;
XX
DR   WPI; 1995-206931/27.
XX
PT   Identifying gene signatures in 3'-directed human cDNA library - e.g.
PT   for diagnosis of abnormal cell function, by preparing cDNA that
PT   reflects relative abundance of corresp. mRNA in specific human
PT   tissues
XX
PS   Claim 1; Page 545; 2245pp; Japanese.
XX
CC   A single-stranded DNA (or its complementary strand or the corresp.
CC   double-stranded DNA) which comprises one of the 7837 "GS" sequences
CC   given in T19001-T26837 and which is able to hybridise to part of
CC   human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
CC   sequences were obtained from 3'-directed cDNA libraries prepared
CC   from various human tissues; synthesis of cDNA was initiated from the
CC   3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
CC   untranslated sequence is unique to a particular mRNA species, almost
CC   all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
CC   is constructed so as to reflect accurately the relative abundance of
CC   different mRNAs in the particular tissue from which it was derived.
CC   The appearance frequency of a given GS in a cDNA library can be
CC   determined (esp. using primers and probes derived from the GS
CC   sequences) as a means of diagnosing abnormal cell function or for
CC   recognising different cell types.
XX
SQ   Sequence 439 BP; 118 A; 77 C; 79 G; 143 T; 22 other;


  Query Match          7.6%;  Score 171;  DB 16;  Length 439;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-53;
  Matches  171;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1764 actgttatattaattgccaatataagtaaatatagattatatatgtatagtgtttcacaa 1823
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     70 actgttatattaattgccaatataagtaaatatagattatatatgtatagtgtttcacaa 129

Qy   1824 agcttagacctttaccttccagccaccccacagtgcttgatatttcagagtcagtcattg 1883
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    130 agcttagacctttaccttccagccaccccacagtgcttgatatttcagagtcagtcattg 189

Qy   1884 gttatacatgtgtagttccaaagcacataagctagaagaagaaatatttct 1934
           |||||||||||||||||||||||||||||||||||||||||||||||||
Db    190 gttatacatgtgtagttccaaagcacataagctagaagaagaaatatttct 240
```

```
RESULT  13
X23499
ID   X23499 standard; DNA; 211 BP.
XX
AC   X23499;
XX
DT   17-JUN-1999  (first entry)
XX
DE   Human neutrophil cDNA clone 921.
XX
KW   Neutrophil; gene expression profile; granulocyte; pathogen-exposed;
KW   sterile inflammatory disease; detection; therapeutic agent; human;
KW   expression modulator; pathogenic infection; cell activation; primer;
KW   global transcriptional response; ss.
XX
OS   Homo sapiens.
XX
PN   WO9910536-A1.
XX
PD   04-MAR-1999.
XX
PF   21-AUG-1998;   98WO-US17284.
XX
PR   22-AUG-1997;   97US-0056844.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   Goguen J,  Newburger P,  Prashar Y,  Weissman SM,  Yerramilli SV;
XX
DR   WPI; 1999-204678/17.
XX
PT   Detection of pathogen exposure or sterile inflammatory disease in a
PT   subject  - by comparing gene expression profiles from granulocytes
PT   of the patient and control granulocytes
XX
PS   Example 3; Page 53; 84pp; English.
XX
CC   This invention describes a method for the comparison of gene expression
CC   profiles from granulocytes from a test subject and from pathogen-exposed
CC   or sterile inflammatory disease granulocytes or quiescent granulocytes.
CC   The method is used to detect pathogen exposure or sterile inflammatory
CC   disease in a subject and to identify therapeutic agents that modulate
CC   expression of a gene in response to a pathogenic infection or to
CC   sterile inflammatory disease in a subject. The method tests for global
CC   transcriptional response of granulocytes during cell activation.
XX
SQ   Sequence 211 BP; 53 A; 37 C; 42 G; 79 T; 0 other;


  Query Match          4.2%;  Score 95;  DB 20;  Length 211;
  Best Local Similarity   100.0%;  Pred. No. 1e-25;
  Matches   95;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1414 aaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatgta 1473
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     34 aaaattacctgtcttgactgccatgtgttcatcatcttaagtattgtaagctgctatgta 93

Qy   1474 tggatttaaaccgtaatcatatctttttcctatct 1508
           |||||||||||||||||||||||||||||||||
Db     94 tggatttaaaccgtaatcatatctttttcctatct 128


RESULT  14
Z09075
ID   Z09075 standard; cDNA; 412 BP.
XX
AC   Z09075;
XX
DT   19-OCT-1999  (first entry)
XX
DE   Differentiation Induction Subtraction Hybridization DISH-846-2 sequence.
XX
KW   DAP; differentiation-associated protein; terminal differentiation;
```

```
KW   growth arrest; differentiation induction subtraction hybridization;
KW   DISH; melanoma; breast; lung; colorectal; prostate; cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9937774-A2.
XX
PD   29-JUL-1999.
XX
PF   25-JAN-1999;   99WO-US01549.
XX
PR   29-MAY-1998;   98US-0087167.
PR   26-JAN-1998;   98US-0073298.
PR   11-FEB-1998;   98US-0074441.
PR   12-MAR-1998;   98US-0077804.
PR   25-MAR-1998;   98US-0079326.
PR   28-APR-1998;   98US-0083195.
PR   15-MAY-1998;   98US-0085609.
PR   26-MAY-1998;   98US-0086829.
XX
PA   (GENQ-) GENQUEST INC.
XX
PI   Fisher PB,  Huang F;
XX
DR   WPI; 1999-479051/40.
XX
PT   Differentiation-associated proteins and related polynucleotides,
PT   useful for vaccine and pharmaceuticals to inhibit cell growth
XX
PS   Claim 1; Fig 66; 144pp; English.
XX
CC   Sequences Z09006-Z09075 are Differentiation Induction Subtraction
CC   Hybridization (DISH) sequences, which encode Differentiation-Associated
CC   Proteins (DAPs). DAPs are associated with terminal differentiation and
CC   growth arrest and the sequences encoding them range from 97-903 base
CC   pairs in length. A DAP, a DAP fragment or a DAP polynucleotide may be
CC   useful in inhibiting the development of cancer including prostate,
CC   breast, lung and colorectal cancer, melanoma, astrocytoma or glioblastoma
CC   multiforme. Determining the level of a DAP or its coding sequence, in a
CC   tumour sample can be used to determine whether the tumour is malignant.
CC   The progression of cancer can be monitored by measuring DAP expression or
CC   activity levels over a period of time. An agent that increases expression
CC   of a DAP can also be used to inhibit the development of cancer.
XX
SQ   Sequence 412 BP; 123 A; 76 C; 80 G; 119 T; 14 other;


  Query Match             3.2%;  Score 71;  DB 20;  Length 412;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-17;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1814 tgtttcacaaagcttagacctttaccttccagccaccccacagtgcttgatatttcagag 1873
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8 tgtttcacaaagcttagacctttaccttccagccaccccacagtgcttgatatttcagag 67

Qy   1874 tcagtcattgg 1884
            ||||||||||
Db     68 tcagtcattgg 78


RESULT  15
Z46327
ID   Z46327 standard; cDNA; 412 BP.
XX
AC   Z46327;
XX
DT   07-MAR-2000  (first entry)
XX
DE   Human differentiation-associated cDNA, DISH-846-2.
XX
KW   Differentiation; terminal; cell cycle arrest; vaccine; inhibition;
KW   proliferation; cancer; tumour; prostate; breast; lung; colorectal;
KW   melanoma; astrocytoma; glioblastoma multiforme; antibody; diagnosis;
KW   malignant; progression; monitoring; identification; modulator;
KW   expression; development; ds.
XX
OS   Homo sapiens.
XX
PN   WO9960124-A2.
XX
PD   25-NOV-1999.
XX
PF   17-MAY-1999;   99WO-US10889.
XX
PR   15-MAY-1998;   98US-0085609.
PR   26-MAY-1998;   98US-0086829.
PR   29-MAY-1998;   98US-0087167.
XX
PA   (HUAN/) HUANG F.
PA   (FISH/) FISHER P B.
XX
PI   Huang F,  Fisher PB;
XX
DR   WPI; 2000-062456/05.
XX
PT   Differentiation-associated sequences, methods for inhibiting cell
PT   growth and inducing differentiation  -
XX
PS   Claim 4; Fig 28; 87pp; English.
XX
CC   Sequences Z46300-Z46327 represent cDNAs encoding human differentiation-
CC   associated proteins which are associated with terminal differentiation
CC   and cell cycle arrest. The cDNAs, or the proteins they encode, can be
CC   used in vaccines or other therapeutic compositions to inhibit development
CC   of cancer, especially prostate, breast, lung and colorectal cancer,
CC   melanoma, astrocytoma or glioblastoma multiforme. Determination of the
CC   level of the differentiation-associated protein (especially using a
CC   monoclonal antibody) is useful for assessing whether a tumour is
CC   malignant. The progression of a cancer can be monitored by comparing
CC   levels of a differentiation-associated nucleotide or protein over a
CC   period of time. The protein can also be used to identify agents that
CC   modulate cell proliferation and/or differentiation. Differentiation-
CC   associated protein gene promoters or regulatory elements can be
CC   operably linked to reporter genes and used in assays to identify agents
CC   that modulate expression. An agent that increases expression of such
CC   proteins is useful for inhibiting the development of a cancer.
XX
SQ   Sequence 412 BP; 123 A; 76 C; 80 G; 119 T; 14 other;


  Query Match             3.2%;  Score 71;  DB 21;  Length 412;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-17;
  Matches   71;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1814 tgtttcacaaagcttagacctttaccttccagccaccccacagtgcttgatatttcagag 1873
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      8 tgtttcacaaagcttagacctttaccttccagccaccccacagtgcttgatatttcagag 67

Qy   1874 tcagtcattgg 1884
            ||||||||||
Db     68 tcagtcattgg 78


Search completed: January 31, 2001, 18:46:54
Job time: 20812 sec
```

THIS PAGE IS BLANK

```
OM of: US-09-544-776-2 to: N_Geneseq_36:*   out_format : pfs

Date: Feb 1, 2001  3:27 AM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool/US09544776/runat_31012001_082320_8189/app_query.fasta_1.435
 -DB=N_Geneseq_36 -QFMT=fastap -SUFFIX=p2n.rng -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
 -QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
 -NORM=ext -MINLEN=0 -MAXLEN=2000000000
 -USER=US09544776_@CGN1_1_131 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
 -WAIT -THREADS=1

Search information block:
Query: US-09-544-776-2
Query length: 373
Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 187831343
Search time (sec): 85.730000


score_list:
Sequence          Strd Orig    ZScore    EScore Len  ! Documentation  ..
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z56888 +  1879.00 1523.05  4.8e-77   1122  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z36230 +  1879.00 1520.50  6.6e-77   1610  ! c
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z56886 +  1459.50 1177.21  8.8e-58   3579  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:A23454 +  1437.00 1158.15  1.0e-56   4093  ! c
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V23695 +   917.00  751.16  4.7e-34    799  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X04379 +   917.00  748.20  6.9e-34   1213  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X97587 +   908.00  742.39  1.5e-33    991  ! Ex
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V30920 +   905.50  734.17  4.2e-33   2386  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:X75770 +   747.50  604.91  6.6e-26   3202  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V59748 +   672.50  548.75  8.9e-23   1766  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V59749 +   659.50  535.38  4.9e-22   2664  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z36240 +   655.00  535.07  5.1e-22   1668  ! c
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z38319 +   655.00  534.70  5.4e-22   1759  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X60810 +   644.50  526.67  1.5e-21   1656  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z38318 +   644.00  532.28  7.4e-22    708  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V23696 +   550.00  453.53  1.8e-17   1095  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V59602 +   541.50  448.97  3.2e-17    794  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1993.DAT:Q61265 +   385.00  327.60  1.9e-10    414  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X41193 +   376.00  320.53  4.6e-10    404  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X41212 +   314.00  270.29  2.9e-07    424  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V23697 +   275.00  242.33  1.0e-05    261  ! Hu
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:Z23778 +   217.00  170.85  0.0997    8705  ! V
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V21683 -   217.00  170.16  0.1089    9600  ! V
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:Z22248 -   217.00  169.61  0.1169   10380  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1993.DAT:Q51731 -   217.00  169.46  0.1191   10596  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1996.DAT:T40348 -   217.00  169.46  0.1191   10596  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X15650 -   217.00  169.46  0.1191   10596  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X90923 +   212.00  170.14  0.1093    5452  ! A
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X90924 -   210.00  175.89  0.0523    1925  ! E
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V55831 -   209.50  181.70  0.0248    799  ! Nu
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V55830 -   204.50  177.71  0.0414    795  ! FI
/SIDS6/gcgdata/geneseq/geneseqn/NA1990.DAT:Q03324 -   191.00  151.92  1.13      6567  ! E
/SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:T89346 +   186.00  152.95  0.9901    3211  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:T89345 +   186.00  151.57  1.18      3901  ! H
/SIDS6/gcgdata/geneseq/geneseqn/NA1986.DAT:N60488 -   184.00  160.62  0.3702    864  ! Ei
/SIDS6/gcgdata/geneseq/geneseqn/NA1990.DAT:Q03317 -   184.00  160.62  0.3702    864  ! cD
/SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:T93610 +   184.00  149.88  1.47      3946  ! M
/SIDS6/gcgdata/geneseq/geneseqn/NA1995.DAT:Q76213 +   183.50  141.62  4.24     12001  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1997.DAT:X83007 +   183.00  130.95  16.64    51259  !
/SIDS6/gcgdata/geneseq/geneseqn/NA1991.DAT:Q14183 -   179.50  149.96  1.45      2338  ! N
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V23249 -   179.50  149.96  1.45      2338
/SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z38195 -   179.50  149.96  1.45      2338
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V22682 -   177.50  148.74  1.70      2214
/SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V22683 -   177.50  145.85  2.46      3331
/SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:Z32021 -   177.50  145.85  2.46      3331

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z56888

seq_documentation_block:
ID   Z56888 standard; DNA; 1122 BP.
XX
AC   Z56888;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human MAGI polypeptide variant encoding DNA.
XX
KW   MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW   spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW   psychiatric disorder; developmental disorder; inflammatory disorder;
KW   stroke; cytostatic; cerebroprotective; neuroprotective; variant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1122
FT                   /*tag= a
FT                   /product= "MAGI polypeptide"
XX
PN   WO200005364-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;   99WO-GB02360.
XX
PR   22-JUL-1998;   98GB-0016024.
PR   19-JUL-1999;   99GB-0016898.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D,  Prinjha RK;
XX
DR   WPI; 2000-182693/16.
DR   P-PSDB; Y56969.
XX
PT   Novel polypeptides related to neuroendocrine-specific proteins and
PT   polynucleotides useful for diagnosis of various diseases and for
PT   treatment of cancer and neurological disorders -
XX
PS   Claim 5; Page 21-22; 35pp; English.
XX
CC   The invention relates to human MAGI protein, which is similar to
CC   neuroendocrine-specific protein. The MAGI protein can be expressed by
CC   standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC   and antibodies are useful for treating diseases, including neuropathies,
CC   spinal injury, neuronal degeneration, neuromuscular disorders,
CC   psychiatric disorders and developmental disorders, cancer, stroke and
CC   inflammatory disorders. The polynucleoitde is also useful for chromosome
CC   localization and for tissue expression studies. The present sequence
CC   represents a DNA encoding the human MAGI protein variant.
XX
SQ   Sequence 1122 BP; 224 A; 339 C; 316 G; 243 T; 0 other;


alignment_scores:
            Quality: 1879.00              Length:    373
              Ratio:  5.078                 Gaps:      0
 Percent Similarity:  99.196   Percent Identity: 99.196

alignment_block:
 US-09-544-776-2 x Z56888   ..

 Align seg 1/1  to: Z56888  from: 1  to: 1122
```

```
  1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProPr 17
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACC 50

 17 oArgProGlnProAlaPheLysTyrGlnPheValArgGluProGluAspG 34
    ||||||||||||||||||||||||||||||||||||||||||||||||||
 51 CCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACG 100

 34 luGluGluGluGluGluGluGluGluAspGluAspGluAspLeuGlu 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 AGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAG 150

 51 GluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAlaPr 67
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 GAGCTGGAGGTGCTGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCC 200

 67 oValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsnA 84
    ||||||||||||||||||||||||||||||||||||||||||||||||||
201 AGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGACTTCGGAAATG 250

 84 spPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
    ||||||||||||||||||||||||||  ||||||||||||||||||||||
251 ACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTC 300

101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVa 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGT 350

117 lProAlaProSerPheLeuSerAlaAlaAlaValSerProSerLysLeuP 134
    ||||||||||||  ||||||||||||||||||||||||||||||||||||
351 GCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCC 400

134 roGluAspAspGluProProAlaArgProProProProProProAlaSer 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
401 CTGAGGACGACGAGCCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGC 450

151 ValSerProGlnAlaGluProValTrpThrProProAlaProAlaProAl 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
451 GTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCGCCAGCCCCGGCTCCCGC 500

167 aAlaProProSerThrProAlaAlaProLysArgArgGlySerSerGlyS 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||
501 CGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCAGGGGCTCCTCGGGCT 550

184 erValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
551 CAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG 600

201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIl 217
    ||||||||||||||||||||||||||||||||||||||||||||||||||
601 GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCAT 650

217 eValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleS 234
    ||||||||||||||||||||||||||||||||||||||||||||||||||
651 TGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCA 700

234 erProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGlu 250
    ||  ||||||||||||||||||||||||||||||||||||||||||||||
701 GCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAA 750

251 GlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGl 267
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 GGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 800

267 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 284
    ||||||||||||||||||||||||||||||||||||||||||||||||||
801 GTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGA 850

284 leLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
851 TAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG 900
```

```
301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAs 317
    ||||||||||||||||||||||||||||||||||||||||||||||||||
901 AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAA 950

317 nGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProV 334
    ||||||||||||||||||||||||||||||||||||||||||||||||||
951 TGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTG 1000

334 alIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1001 TTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCA 1050

351 AsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGl 367
    ||||||||||||||||||||||||||||||||||||||||||||||||||
1051 AATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGG 1100

367 yLeuLysArgLysAlaGlu 373
    ||||||||||||||||||
1101 ATTGAAGCGCAAAGCTGAA 1119
```

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z36230

seq_documentation_block:

```
ID   Z36230 standard; cDNA; 1610 BP.
XX
AC   Z36230;
XX
DT   22-FEB-2000  (first entry)
XX
DE   cDNA encoding a bone marrow secreted protein designated BMS112.
XX
KW   Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW   cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW   myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW   erythroid progenitor cell; colony stimulating factor; granulocyte;
KW   monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW   platelet disorder; thrombocytopenia; hematopoeitic stem cell;
KW   stem cell disorder; aplastic anaemia; bone differentiation;
KW   paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW   ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW   bone fracture; cartilage damage; artificial joint; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             132..1253
FT                   /*tag=  a
FT                   /product= "bone marrow secreted protein"
FT   polyA_signal    1516..1521
FT                   /*tag=  b
XX
PN   WO9933979-A2.
XX
PD   08-JUL-1999.
XX
PF   18-DEC-1998;   98WO-US27008.
XX
PR   30-DEC-1997;   97US-0068958.
PR   24-SEP-1998;   98US-0101603.
PR   30-SEP-1998;   98US-0102540.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Lin H,  Cao L;
XX
DR   WPI; 2000-038344/03.
DR   P-PSDB; Y53624.
XX
PT   New isolated human polynucleotide and secreted proteins can induce
PT   production of other cytokines in certain cell populations -
XX
PS   Claim 11; Page 72-74; 120pp; English.
XX
```

```
CC   Z36228-49 encode bone marrow secreted proteins of human bone marrow
CC   stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC   cell differentiation activity (either inducing or inhibiting). They can
CC   be used to support colony forming cells or factor-dependent cell lines,
CC   to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC   deficiencies. In addition, they may be used to support the growth and
CC   proliferation of erythroid progenitor cells, and to treat various
CC   anaemias. They can have colony stimulating factor (CSF) activity and can
CC   be used to support the growth and proliferation of myeloid cells such as
CC   granulocytes, monocytes or macrophages, to prevent or treat
CC   myelo-suppression, to support the growth and proliferation of
CC   megakaryocytes and platelets, thereby allowing prevention or treatment
CC   of platelet disorders such as thrombocytopenia, to support the growth
CC   and proliferation of hematopoeitic stem cells, either in place of or in
CC   conjunction with platelet transfusions, to treat stem cell disorders,
CC   such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC   repopulate the stem cell compartment after irradiation or chemotherapy.
CC   They can be used for growth or differentiation of bone, cartilage,
CC   tendon, ligament, or nerve tissue, as well as for wound healing and
CC   tissue repair and replacement, and in the treatment of burns, incisions
CC   and ulcers, to induce cartilage and/or bone growth in circumstances where
CC   bone is not normally formed and thus have an application in healing bone
CC   fractures and cartilage damage or defects, prophylactic use in fracture
CC   reduction and also in the improved fixation of artificial joints.
XX
SQ   Sequence 1610 BP; 354 A; 458 C; 426 G; 372 T; 0 other;


alignment_scores:
            Quality: 1879.00              Length:    373
              Ratio:  5.078                Gaps:      0
 Percent Similarity:  99.196   Percent Identity: 99.196

alignment_block:
 US-09-544-776-2 x Z36230   ..

 Align seg 1/1  to: Z36230  from: 1  to: 1610

       1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProPr 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     132 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACC 181

      17 oArgProGlnProAlaPheLysTyrGlnPheValArgGluProGluAspG 34
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     182 CCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACG 231

      34 luGluGluGluGluGluGluGluGluAspGluAspGluAspLeuGlu 50
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     232 AGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAG 281

      51 GluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAlaPr 67
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     282 GAGCTGGAGGTGCTGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCC 331

      67 oValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsnA 84
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     332 AGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGACTTCGGAAATG 381

      84 spPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
         ||||||||||||||||||||||||   ||||||||||||||||||||||||
     382 ACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTC 431

     101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVa 117
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     432 GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGT 481

     117 lProAlaProSerPheLeuSerAlaAlaAlaValSerProSerLysLeuP 134
         ||||||||||||   ||||||||||||||||||||||||||||||||||||
     482 GCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCC 531

     134 roGluAspAspGluProProAlaArgProProProProProProAlaSer 150
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     532 CTGAGGACGACGAGCCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGC 581

     151 ValSerProGlnAlaGluProValTrpThrProProAlaProAlaProAl 167
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     582 GTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCGCCAGCCCCGGCTCCCGC 631

     167 aAlaProProSerThrProAlaAlaProLysArgArgGlySerSerGlyS 184
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     632 CGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCAGGGGCTCCTCGGGCT 681

     184 erValValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyVal 200
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     682 CAGTGGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG 731

     201 ValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIl 217
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     732 GTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCAT 781

     217 eValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleS 234
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     782 TGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCA 831

     234 erProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGlu 250
         ||   ||||||||||||||||||||||||||||||||||||||||||||||
     832 GCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAA 881

     251 GlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGl 267
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     882 GGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGA 931

     267 uLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrI 284
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     932 GTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTCAACTGCACGA 981

     284 leLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeu 300
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     982 TAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTG 1031

     301 LysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAs 317
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1032 AAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAA 1081

     317 nGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProV 334
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1082 TGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTG 1131

     334 alIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAla 350
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1132 TTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCA 1181

     351 AsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGl 367
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1182 AATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGG 1231

     367 yLeuLysArgLysAlaGlu 373
         ||||||||||||||||||
    1232 ATTGAAGCGCAAAGCTGAA 1250

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z56886

seq_documentation_block:
ID   Z56886 standard; DNA; 3579 BP.
XX
AC   Z56886;
XX
DT   25-APR-2000  (first entry)
XX
DE   Human MAGI polypeptide encoding DNA.
XX
KW   MAGI protein; neuroendocrine-specific protein; neuropathy; human;
KW   spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
KW   psychiatric disorder; developmental disorder; inflammatory disorder;
KW   stroke; cytostatic; cerebroprotective; neuroprotective; ds.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..3579
FT                   /*tag= a
FT                   /product= "MAGI polypeptide"
XX
PN   WO200005364-A1.
XX
PD   03-FEB-2000.
XX
PF   21-JUL-1999;   99WO-GB02360.
XX
PR   22-JUL-1998;   98GB-0016024.
PR   19-JUL-1999;   99GB-0016898.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Michalovich D,  Prinjha RK;
XX
DR   WPI; 2000-182693/16.
DR   P-PSDB; Y56967.
XX
PT   Novel polypeptides related to neuroendocrine-specific proteins and
PT   polynucleotides useful for diagnosis of various diseases and for
PT   treatment of cancer and neurological disorders -
XX
PS   Claim 5; Page 19-20; 35pp; English.
XX
CC   The invention relates to human MAGI protein, which is similar to
CC   neuroendocrine-specific protein. The MAGI protein can be expressed by
CC   standard recombinant methodology. The MAGI polypeptides, polynucleotides
CC   and antibodies are useful for treating diseases, including neuropathies,
CC   spinal injury, neuronal degeneration, neuromuscular disorders,
CC   psychiatric disorders and developmental disorders, cancer, stroke and
CC   inflammatory disorders. The polynucleoitde is also useful for chromosome
CC   localization and for tissue expression studies. The present sequence
CC   represents a DNA encoding the human MAGI protein.
XX
SQ   Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 other;


alignment_scores:
            Quality: 1459.50              Length:   1192
              Ratio:  3.945                Gaps:      1
 Percent Similarity:  31.040   Percent Identity: 31.040

alignment_block:
 US-09-544-776-2 x Z56886   ..

 Align seg 1/1  to: Z56886  from: 1  to: 3579

       1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProPr 17
         |||||||||||||||||||||||||||||||||||||||||||||||||||
       1 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACC 50

      17 oArgProGlnProAlaPheLysTyrGlnPheValArgGluProGluAspG 34
         |||||||||||||||||||||||||||||||||||||||||||||||||||
      51 CCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACG 100

      34 luGluGluGluGluGluGluGluGluAspGluAspGluAspLeuGlu 50
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     101 AGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAG 150

      51 GluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAlaPr 67
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     151 GAGCTGGAGGTGCTGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCC 200

      67 oValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsnA 84
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     201 AGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGACTTCGGAAATG 250

      84 spPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
         |||||||||||||||||||||||||   |||||||||||||||||||||
     251 ACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTC 300

     101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVa 117
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     301 GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGT 350

     117 lProAlaProSerPheLeuSerAlaAlaAlaValSerProSerLysLeuP 134
         |||||||||||||   |||||||||||||||||||||||||||||||||||
     351 GCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCC 400

     134 roGluAspAspGluProProAlaArgProProProProProProAlaSer 150
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     401 CTGAGGACGACGAGCCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGC 450

     151 ValSerProGlnAlaGluProValTrpThrProProAlaProAlaProAl 167
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     451 GTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCGCCAGCCCCGGCTCCCGC 500

     167 aAlaProProSerThrProAlaAlaProLysArgArgGlySerSerGlyS 184
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     501 CGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCAGGGGCTCCTCGGGCT 550

     184 erVal..................................................  185
         |||||
     551 CAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCTGTGATA 600

     185 ..................................................  185

     601 CGCTCCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACACTAT 650

     185 ..................................................  185

     651 TTCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTT 700

     185 ..................................................  185

     701 CTCTTCCTTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAA 750

     185 ..................................................  185

     751 TACCTTGGTAATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGA 800

     185 ..................................................  185

     801 AAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCAAAAACTCTAC 850

     185 ..................................................  185

     851 TCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATG 900

     185 ..................................................  185

     901 GGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGC 950

     185 ..................................................  185

     951 AAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGT 1000

     185 ..................................................  185

    1001 TAGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTT 1050

     185 ..................................................  185

    1051 ACTAAATTGGTTAAAGAGGATGAAGTTGTGTCTTCAGAAAAAGCAAAAGA 1100

     185 ..................................................  185

    1101 CAGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATGAGGGAGGAAT 1150

     185 ..................................................  185
```

```
1151 ATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATAGTAAG 1200
 185 ..................................................  185
1201 GAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGA 1250
 185 ..................................................  185
1251 AAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATC 1300
 185 ..................................................  185
1301 ACGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACG 1350
 185 ..................................................  185
1351 CCAGAAGGTATAAAGGATCGTCCAGGAGCATATATCACATGTGCTCCCTT 1400
 185 ..................................................  185
1401 TAACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTTCCTTTGTTAG 1450
 185 ..................................................  185
1451 GAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAATAGAAGAAAAG 1500
 185 ..................................................  185
1501 AAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCC 1550
 185 ..................................................  185
1551 TTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATA 1600
 185 ..................................................  185
1601 ATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTG 1650
 185 ..................................................  185
1651 ACTCCAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTAC 1700
 185 ..................................................  185
1701 TGGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTTCAAACATCAG 1750
 185 ..................................................  185
1751 AAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTT 1800
 185 ..................................................  185
1801 GAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGA 1850
 185 ..................................................  185
1851 AGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGC 1900
 185 ..................................................  185
1901 CCAGCTCATCACCATTAGAAGCTTCTTCAGTTAATTATGAAAGCATAAAA 1950
 185 ..................................................  185
1951 CATGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACT 2000
 185 ..................................................  185
2001 AAAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTA 2050
 185 ..................................................  185
2051 ATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGAT 2100
 185 ..................................................  185
2101 TTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGA 2150
 185 ..................................................  185
2151 TTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGC 2200
 185 ..................................................  185
2201 TAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGAT 2250
 185 ..................................................  185
2251 GATTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGT 2300
 185 ..................................................  185
2301 GAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATAGAATATGAAA 2350
 185 ..................................................  185
2351 ATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAGCCATATTTG 2400
 185 ..................................................  185
2401 GAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGA 2450
 185 ..................................................  185
2451 TGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGG 2500
 185 ..................................................  185
2501 AGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAA 2550
 185 ..................................................  185
2551 GCACAGATAAGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAAT 2600
 185 ..................................................  185
2601 TATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGATTCATTTTCTA 2650
 185 ..................................................  185
2651 AATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATT 2700
 185 ..................................................  185
2701 GCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCA 2750
 185 ..................................................  185
2751 TGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTT 2800
 185 ..................................................  185
2801 TCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTA 2850
 185 ..................................................  185
2851 TTGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCAT 2900
 185 ..................................................  185
2901 AGTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCG 2950
 185 ..................................................  185
2951 ATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTG 3000
```

```
 186 ............ValValAspLeuLeuTyrTrpArgAspIleLysLysTh 198
                  ||||||||||||||||||||||||||||||||||||||||
3001 AGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGAC 3050

 198 rGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValP 215
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3051 TGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTAT 3100

 215 heSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerVal 231
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3101 TCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTG 3150

 232 ThrIleSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSe 248
     |||||||||    ||||||||||||||||||||||||||||||||||||
3151 ACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATC 3200

 248 rAspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleS 265
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3201 AGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATAT 3250

 265 erGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsn 281
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3251 CTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAC 3300

 282 CysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAs 298
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3301 TGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGA 3350

 298 pSerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaL 315
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3351 TTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCT 3400

 315 euPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSer 331
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3401 TGTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGT 3450

 332 ValProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGl 348
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3451 GTTCCTGTTATTTATGAACGGCATCAGGCGCAGATAGATCATTATCTAGG 3500

 348 yLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysI 365
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3501 ACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAA 3550

 365 leProGlyLeuLysArgLysAlaGlu 373
     |||||||||||||||||||||||||
3551 TCCCTGGATTGAAGCGCAAAGCTGAA 3576
```

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:A23454

seq_documentation_block:

```
ID   A23454 standard; cDNA; 4093 BP.
XX
AC   A23454;
XX
DT   19-JUN-2000  (first entry)
XX
DE   cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW   Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW   blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW   infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW   neurodegenerative disease; asthma; contraceptive; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1048..3729
FT                   /*tag= a
FT                   /product= "Human secreted protein vb22_1"
FT   CDS             152..1006
FT                   /*tag= b
FT                   /product= "Clone vb22_1 ORF2"
XX
PN   WO200011015-A1.
XX
PD   02-MAR-2000.
XX
PF   24-AUG-1999;   99WO-US19351.
XX
PR   24-AUG-1998;   98US-0097638.
PR   24-AUG-1998;   98US-0097659.
PR   09-SEP-1998;   98US-0099618.
PR   28-SEP-1998;   98US-0102092.
PR   25-NOV-1998;   98US-0109978.
PR   23-DEC-1998;   98US-0113645.
PR   23-DEC-1998;   98US-0113646.
PR   23-AUG-1999;   99US-0379246.
XX
PA   (ALPH-) ALPHAGENE INC.
XX
PI   Valenzuela D,  Yuan O,  Hoffman H,  Hall J,  Rapiejko P;
XX
DR   WPI; 2000-224657/19.
DR   P-PSDB; Y95012, Y95030.
XX
PT   New secreted or transmembrane proteins and polynucleotides encoding
PT   them, useful for treating neurodegenerative disorders, autoimmune
PT   diseases and cancer -
XX
PS   Claim 72; Page 321-322; 357pp; English.
XX
CC   The invention relates to 40 human secreted proteins (Y94981-Y95020),
CC   and cDNA sequences encoding them (A23423-A23462). The secreted proteins
CC   of the invention include those that are thought to be only partially
CC   secreted, i.e., transmembrane proteins. The proteins of the invention may
CC   exhibit one or more activities selected from the following: cytokine
CC   activity; cell proliferation; differentiation; immune modulation;
CC   haematopoiesis regulation; tissue growth activity; activin/inhibin
CC   activity; chemotactic/chemokinetic activity; haemostatic and
CC   thrombolytic activity; anti-inflammatory activity; and tumour inhibition
CC   activity. The proteins may be administered to patients as vaccines, and
CC   the nucleotides may be used as part of a gene therapy regime. Diseases or
CC   conditions that may be treated using the proteins or nucleotides of the
CC   invention include autoimmune diseases; genetic disorders; haemophilia;
CC   cardiovascular diseases; cancer; bacterial, fungal and viral infections,
CC   especially HIV; multiple sclerosis; rheumatoid arthritis; pulmonary
CC   inflammation; Guillain-Barre syndrome; insulin dependent diabetes
CC   mellitus; and allergic reactions such as asthma and anaemia. They may
CC   also be used for treating wounds, burns, ulcers, osteoporosis,
CC   osteoarthritis, periodontal diseases, Alzheimer's disease, Parkinson's
CC   disease, Huntington's disease and amyotrophic lateral sclerosis (ALS).
CC   Proteins with activin/inhibin activity may additionally be useful as
CC   contraceptives. Nucleic acid sequences of the invention may be used in
CC   chromosome mapping, and as a source of diagnostic primers and probes.
CC   The present sequence represents cDNA encoding one of the 40 proteins of
CC   the invention.
XX
SQ   Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 other;
```

alignment_scores:

```
            Quality: 1437.00              Length:   1192
              Ratio:  3.884                 Gaps:      2
 Percent Similarity:  31.040   Percent Identity: 30.956
```

alignment_block:

```
 US-09-544-776-2 x A23454    ..

 Align seg 1/1  to: A23454  from: 1  to: 4093

       1 MetGluAspLeuAspGlnSerProLeuValSerSerSerAspSerProPr 17
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     152 ATGGAAGACCTGGACCAGTCTCCTCTGGTCTCGTCCTCGGACAGCCCACC 201

      17 oArgProGlnProAlaPheLysTyrGlnPheValArgGluProGluAspG 34
```

```
    ||||||||||||||||||||||||||||||||||||||||||||||||||
202 CCGGCCGCAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACG 251

 34 luGluGluGluGluGluGluGluGluAspGluAspGluAspLeuGlu 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
252 AGGAGGAAGAAGAGGAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAG 301

 51 GluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAlaPr 67
    ||||||||||||||||||||||||||||||||||||||||||||||||||
302 GAGCTGGAGGTGCTGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCC 351

 67 oValProThrAlaProAlaAlaGlyAlaProLeuMetAspPheGlyAsnA 84
    ||||||||||||||||||||||||||||||||||||||||||||||||||
352 AGTGCCCACCGCCCCTGCCGCCGGCGCGCCCCTGATGGACTTCGGAAATG 401

 84 spPheValProProAlaProArgGlyPheLeuProAlaAlaProProVal 100
    ||||||||||||||||||||||||  ||||||||||||||||||||||||
402 ACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCCCCCGTC 451

101 AlaProGluArgGlnProSerTrpAspProSerProValSerSerThrVa 117
    ||||||||||||||||||||||||||||||||||||||||||||||||||
452 GCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGT 501

117 lProAlaProSerPheLeuSerAlaAlaAlaValSerProSerLysLeuP 134
    ||||||||||||||  ||||||||||||||||||||||||||||||||||
502 GCCCGCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCC 551

134 roGluAspAspGluProProAlaArgProProProProProProAlaSer 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
552 CTGAGGACGACGAGCCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGC 601

151 ValSerProGlnAlaGluProValTrpThrProProAlaProAlaProAl 167
    ||||||||||||||||||||||||||||||||||||||||||||||||||
602 GTGAGCCCCCAGGCAGAGCCCGTGTGGACCCCGCCAGCCCCGGCTCCCGC 651

167 aAlaProProSerThrProAlaAlaProLysArgArgGlySerSerGlyS 184
    ||||||||||||||||||||||||||||||||||||||||||||||||||
652 CGCGCCCCCCTCCACCCCGGCCGCGCCCAAGCGCAGGGGCTCCTCGGGCT 701

184 er..................................................  184
    ||
702 CAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCTGTGATA 751

184 ..................................................  184

752 CGCTCCTCTGCAGAAAATATGGACTTGAAGGAGCAGCCAGGTAACACTAT 801

184 ..................................................  184

802 TTCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTT 851

184 ..................................................  184

852 CTCTTCCTTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAA 901

184 ..................................................  184

902 TACCTTGGTAATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGA 951

184 ..................................................  184

952 AAATGTCAGTGAAGCTTCTAAAGAGGTCTCAGAGAAGGCAAAACTCTACT 1001

184 ..................................................  184

1002 CATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATACTCAGAAATGG 1051

184 ..................................................  184

1052 GATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1101

184 ..................................................  184

1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTT 1151

184 ..................................................  184

1152 AGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTA 1201

184 ..................................................  184

1202 CTAAATTGGTTAAAGAGGATGAAGTTGTGTCTTCAGAAAAAGCAAAAGAC 1251

184 ..................................................  184

1252 AGTTTTAATGAAAAGAGAGTTGCAGTGGAAGCTCCTATGAGGGAGGAATA 1301

184 ..................................................  184

1302 TGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAAGATAGTAAGG 1351

184 ..................................................  184

1352 AAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTGGAA 1401

184 ..................................................  184

1402 AGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCA 1451

184 ..................................................  184

1452 CGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGC 1501

184 ..................................................  184

1502 CAGAAGGTATAAAGGATCGTTCAGGAGCATATATCACATGTGCTCCCTTT 1551

184 ..................................................  184

1552 AACCCAGCAGCAACTGAGAGCATTGCAACAAACATTTTTCCTTTGTTAGG 1601

184 ..................................................  184

1602 AGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAATAGAAGAAAAGA 1651

184 ..................................................  184

1652 AGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAACCCT 1701

184 ..................................................  184

1702 TTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAA 1751

184 ..................................................  184

1752 TTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGA 1801

184 ..................................................  184

1802 CTCCAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACT 1851

184 ..................................................  184

1852 GGTACAAAGATTGCTTATGAAACAAAAATGGACTTGGTTCAAACATCAGA 1901

184 ..................................................  184

1902 AGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTTTGCCCATCATTTG 1951

184 ..................................................  184

1952 AAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATGGAA 2001

184 ..................................................  184

2002 GCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCC 2051
```

```
 184 ..................................................  184
2052 CAGCTCATCACCATTAGAAGCTTCTTCAGTTAATTATGAAAGCATAAAAC 2101
 184 ..................................................  184
2102 ATGAGCCTGAAAACCCCCCCACCATATGAAGAGGCCATGAGTGTATCACTA 2151
 184 ..................................................  184
2152 AAAAAAGTATCAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAA 2201
 184 ..................................................  184
2202 TGCAGCTCTTCAAGAAACAGAAGCTCCTTATATATCTATTGCATGTGATT 2251
 184 ..................................................  184
2252 TAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTCTCTGAT 2301
 184 ..................................................  184
2302 TATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCT 2351
 184 ..................................................  184
2352 AGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATG 2401
 184 ..................................................  184
2402 ATTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTG 2451
 184 ..................................................  184
2452 AAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAA 2501
 184 ..................................................  184
2502 TAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGAGGAAAGCCATATTTGG 2551
 184 ..................................................  184
2552 AATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT 2601
 184 ..................................................  184
2602 GAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGA 2651
 184 ..................................................  184
2652 GCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAG 2701
 184 ..................................................  184
2702 CACAGATAAGAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATT 2751
 184 ..................................................  184
2752 ATAGATGAGTTCCCTACATTGATCAGTTCTAAAACTGATTCATTTTCTAA 2801
 184 ..................................................  184
2802 ATTAGCCAGGGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATTG 2851
 184 ..................................................  184
2852 CTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCAT 2901
 184 ..................................................  184
2902 GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTT 2951
```

```
 184 ..................................................  184
2952 CTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTAT 3001
 184 ..................................................  184
3002 TGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATA 3051
 184 ..................................................  184
3052 GTTAAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGA 3101
 184 ..................................................  184
3102 TACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTGA 3151
 185 ......Val..ValValAspLeuLeuTyrTrpArgAspIleLysLysThr 198
           :::  ||||||||||||||||||||||||||||||||||||||||
3152 GTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT 3201
 199 GlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPh 215
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3202 GGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATT 3251
 215 eSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValT 232
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3252 CAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA 3301
 232 hrIleSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSer 248
     ||||||||   ||||||||||||||||||||||||||||||||||||||||
3302 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCA 3351
 249 AspGluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSe 265
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3352 GATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 3401
 265 rGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnC 282
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3402 TGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACT 3451
 282 ysThrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAsp 298
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3452 GCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 3501
 299 SerLeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLe 315
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3502 TCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTT 3551
 315 uPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerV 332
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3552 GTTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 3601
 332 alProValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGly 348
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3602 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGA 3651
 349 LeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIl 365
     ||||||||||||||||||||||||||||||||||||||||||||||||||
3652 CTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAAT 3701
 365 eProGlyLeuLysArgLysAlaGlu 373
     |||||||||||||||||||||||||
3702 CCCTGGATTGAAGCGCAAAGCTGAA 3726
```

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V23695

seq_documentation_block:
ID V23695 standard; cDNA; 799 BP.
XX
AC V23695;
XX
DT 24-JUL-1998 (first entry)
XX

```
DE   Human NSPLP protein A coding sequence.
XX
KW   NSPLP; neuroendocrine-specific protein-like protein; human; gene therapy;
KW   neurodegenerative disease; amyotrophic lateral sclerosis; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             75..674
FT                   /*tag= a
FT                   /product= NSPLPA
XX
PN   WO9806841-A2.
XX
PD   19-FEB-1998.
XX
PF   24-JUL-1997;   97WO-US13469.
XX
PR   12-AUG-1996;   96US-0700607.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Bandman O,  Goli SK,  Hillman J;
XX
DR   WPI; 1998-159533/14.
DR   P-PSDB; W53947.
XX
PT   Human neuro-endocrine-specific protein-like proteins - useful for
PT   diagnosis, monitoring and treatment of cancer and neuro-degenerative
PT   disease
XX
PS   Claim 3; Page 38-39; 73pp; English.
XX
CC   This sequence encodes a human neuroendocrine-specific protein-like
CC   protein (NSPLP) of the invention. Recombinant cells transformed with the
CC   DNA are used to express the NSPLP proteins, which are used to treat
CC   cancer and neurodegenerative diseases such as amyotrophic lateral
CC   sclerosis. Also antisense nucleic acids and antagonists of NSPLP can be
CC   used to inhibit activity of the NSPLP proteins. Antibodies specific for
CC   NSPLP are used for diagnosis and monitoring treatment of diseases
CC   associated with NSPLP expression, in usual immunoassays, and to isolate
CC   NSPLP from natural sources. The NSPLP proteins, or their fragments can
CC   also be used in drug screening to identify NSPLP antagonists. The nucleic
CC   acid can be used diagnostically and for monitoring treatment (in
CC   hybridisation or amplification assays); to isolate closely related
CC   sequences; in gene therapy for both sense and antisense applications
CC   (including use of ribozymes) and for mapping the natural genomic
CC   sequence.
XX
SQ   Sequence 799 BP; 218 A; 141 C; 196 G; 242 T; 2 other;


alignment_scores:
            Quality:  917.00              Length:    188
              Ratio:  4.904                Gaps:      0
 Percent Similarity:  99.468   Percent Identity: 99.468

alignment_block:
 US-09-544-776-2 x V23695   ..

 Align seg 1/1  to: V23695  from: 1  to: 799

     186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPh 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     108 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTT 157

     202 eGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValS 219
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     158 TGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGA 207

     219 erValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPro 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     208 GCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 257

     236 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHi 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     258 AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCA 307

     252 sProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuV 269
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     308 CCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGG 357

     269 alGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     358 TTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 407

     286 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPh 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     408 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTT 457

     302 eAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyL 319
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     458 TGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTC 507

     319 euThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     508 TGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATT 557

     336 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLy 352
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     558 TATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAA 607

     352 sAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuL 369
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     608 GAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGA 657

     369 ysArgLysAlaGlu 373
         |||||||||||||
     658 AGCGCAAAGCTGAA 671

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X04379

seq_documentation_block:
ID   X04379 standard; DNA; 1213 BP.
XX
AC   X04379;
XX
DT   13-APR-1999  (first entry)
XX
DE   Human secreted protein gene 69 clone HAGFT48.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9856804-A1.
XX
PD   17-DEC-1998.
XX
PF   11-JUN-1998;   98WO-US12125.
XX
PR   02-OCT-1997;   97US-0061060.
PR   13-JUN-1997;   97US-0049547.
PR   13-JUN-1997;   97US-0049548.
PR   13-JUN-1997;   97US-0049549.
PR   13-JUN-1997;   97US-0049550.
PR   13-JUN-1997;   97US-0049606.
PR   13-JUN-1997;   97US-0049607.
PR   13-JUN-1997;   97US-0049608.
```

```
PR   13-JUN-1997;   97US-0049609.
PR   13-JUN-1997;   97US-0049610.
PR   13-JUN-1997;   97US-0049611.
PR   13-JUN-1997;   97US-0050566.
PR   13-JUN-1997;   97US-0050901.
PR   13-JUN-1997;   97US-0052989.
PR   08-JUL-1997;   97US-0051919.
PR   18-AUG-1997;   97US-0055984.
PR   12-SEP-1997;   97US-0058665.
PR   12-SEP-1997;   97US-0058668.
PR   12-SEP-1997;   97US-0058669.
PR   12-SEP-1997;   97US-0058750.
PR   12-SEP-1997;   97US-0058971.
PR   12-SEP-1997;   97US-0058972.
PR   12-SEP-1997;   97US-0058975.
PR   02-OCT-1997;   97US-0060834.
PR   02-OCT-1997;   97US-0060841.
PR   02-OCT-1997;   97US-0060844.
PR   02-OCT-1997;   97US-0060865.
PR   02-OCT-1997;   97US-0061059.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Brewer LA,  Ebner R,  Ferrie AM,  Feng P,  Greene JM,  Lafleur DW;
PI   Moore PA,  Ni J,  Olsen HS,  Rosen CA,  Ruben SM,  Shi Y,  Young P;
PI   Yu GL;
XX
DR   WPI; 1999-080881/07.
DR   P-PSDB; W78194.
XX
PT   New isolated human genes and the secreted polypeptides they encode -
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
XX
PS   Claim 1; Page 235-236; 380pp; English.
XX
CC   This sequence represents a nucleic acid molecule which encodes a secreted
CC   human protein.  The gene number, and the clone it is derived from, are
CC   detailed in the descriptor line.  The gene can be used to generate fusion
CC   proteins by linking to the gene to a human immunoglobulin Fc portion
CC   (e.g. X04302) for increasing the stability of the fused protein as
CC   compared to the human protein only.
CC   The invention relates to 86 novel genes and their fragments (nucleic acid
CC   sequences: X04311-X04410; amino acid sequences W78126-W78225) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 86 polynucleotides, based on
CC   which tissues they are most highly expressed in (see X04311 for described
CC   uses).
XX
SQ   Sequence 1213 BP; 335 A; 222 C; 297 G; 355 T; 4 other;


alignment_scores:
            Quality:  917.00              Length:    188
              Ratio:  4.904                 Gaps:      0
 Percent Similarity:  99.468   Percent Identity: 99.468

alignment_block:
 US-09-544-776-2 x X04379   ..

 Align seg 1/1  to: X04379  from: 1  to: 1213

     186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPh 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     248 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTT 297

     202 eGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValS 219
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     298 TGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGA 347

     219 erValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPro 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     348 GCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 397

     236 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHi 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     398 AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCA 447

     252 sProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuV 269
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     448 CCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGG 497

     269 alGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     498 TTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 547

     286 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPh 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     548 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTT 597

     302 eAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyL 319
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     598 TGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTC 647

     319 euThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     648 TGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATT 697

     336 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLy 352
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     698 TATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAA 747

     352 sAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuL 369
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     748 GAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGA 797

     369 ysArgLysAlaGlu 373
         |||||||||||||
     798 AGCGCAAAGCTGAA 811

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X97587

seq_documentation_block:
ID   X97587 standard; DNA; 991 BP.
XX
AC   X97587;
XX
DT   13-SEP-1999  (first entry)
XX
DE   Extended human secreted protein coding sequence, SEQ ID NO. 51.
XX
KW   Secreted protein; human; cytokine; cellular proliferation; cell movement;
KW   cellular differentiation; immune system regulator; anti-inflammatory;
KW   haematopoiesis regulator; tissue growth regulator; tumour inhibitor;
KW   reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
KW   genetic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO9931236-A2.
XX
PD   24-JUN-1999.
XX
PF   17-DEC-1998;   98WO-IB02122.
XX
PR   10-AUG-1998;   98US-0096116.
PR   17-DEC-1997;   97US-0069957.
PR   09-FEB-1998;   98US-0074121.
PR   13-APR-1998;   98US-0081563.
XX
PA   (GEST ) GENSET.
XX
PI   Bougueleret L,  Duclert A,  Dumas Milne Edwards J;
```

```
XX
DR   WPI; 1999-385906/32.
DR   P-PSDB; Y35903.
XX
PT   New isolated human secreted proteins
XX
PS   Claim 1; Page 185-186; 516pp; English.
XX
CC   This sequence represents an extended human secreted protein coding
CC   sequence of the invention. The secreted proteins can be used in treating
CC   or controlling a variety of human conditions. The secreted proteins may
CC   act as cytokines or may affect cellular proliferation or differentiation
CC   or may act as immune system regulators, haematopoiesis regulators, tissue
CC   growth regulators, regulators of reproductive hormones or cell movement
CC   or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or
CC   tumour inhibition activity. The DNAs can be used in forensic procedures
CC   to identify individuals or in diagnostic procedures to identify
CC   individuals having genetic diseases resulting from abnormal expression of
CC   the genes corresponding to the extended cDNAs. They are also useful for
CC   constructing a high resolution map of the human chromosomes. They can
CC   also be used for gene therapy to control or treat genetic diseases.
XX
SQ   Sequence 991 BP; 280 A; 175 C; 232 G; 304 T; 0 other;


alignment_scores:
            Quality:  908.00              Length:    188
              Ratio:  4.882                Gaps:      0
 Percent Similarity:  98.936   Percent Identity: 98.936

alignment_block:
 US-09-544-776-2 x X97587    ..

 Align seg 1/1  to: X97587  from: 1  to: 991

     186 ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPh 202
         ||||||||||||||||||||||||||||||||||||||||||||||||||
      68 GTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTT 117

     202 eGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValS 219
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     118 TGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGCATTGTGA 167

     219 erValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerPro 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     168 GCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT 217

     236 ArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHi 252
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     218 AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCA 267

     252 sProPheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuV 269
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     268 CCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGG 317

     269 alGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLys 285
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     318 TTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 367

     286 GluLeuArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPh 302
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     368 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTT 417

     302 eAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyL 319
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     418 TGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTC 467

     319 euThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIle 335
         ||||||||||||||||||||||||||||||||||||||||||||||||||
     468 TGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATT 517

     336 TyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLy 352
         ||||||||||||||||||||||||||||||||||   ||||||||||||
     518 TATGAACGGCATCAGGCACAGATAGATCATTATCTAGTACTTGCAAATAA 567

     352 sAsnValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeuL 369
         |||||||||||||||||||||||||||||||||||||||||||||||||||
     568 GAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGA 617

     369 ysArgLysAlaGlu 373
         |||||||||||||
     618 AGCGCAAAGCTGAA 631

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V30920

seq_documentation_block:
ID   V30920 standard; cDNA; 2386 BP.
XX
AC   V30920;
XX
DT   14-SEP-1998  (first entry)
XX
DE   Human secreted protein BG160_1 cDNA.
XX
KW   BG160_1; secreted protein; protein factor; human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             102..2030
FT                   /*tag= a
FT   sig_peptide     1863..1899
FT                   /*tag= b
FT                   /note= "putative leader/signal peptide"
FT   mat_peptide     1900..2027
FT                   /*tag= c
XX
PN   WO9817687-A2.
XX
PD   30-APR-1998.
XX
PF   24-OCT-1997;   97WO-US19590.
XX
PR   24-OCT-1997;   97US-0740274.
PR   25-OCT-1996;   96US-0740274.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1998-261426/23.
DR   P-PSDB; W58383.
XX
PT   Nucleic acid encoding secreted protein from human cells - useful,
PT   e.g. as immunomodulator, antitumour agent, promoters of tissue
PT   growth, haemostatic and thrombolytic agents etc.
XX
PS   Claim 20; Page 74-75; 114pp; English.
XX
CC   This cDNA clone, designated BG160_1, codes for a novel human
CC   secreted protein (see W58383).  It was isolated from a human adult
CC   brain cDNA library using methods selective for cDNAs that encode
CC   secreted proteins.  The clone is deposited in composite clone
CC   ATCC 98232; an oligonucleotide (see T99725) is designed to isolate
CC   the clone from the composite.  The predicted AT415_4 amino acid
CC   sequence shows homology to neuroendocrine-specific proteins.  Novel
CC   cDNA clones (see V30916-32) coding for human secreted proteins (see
CC   W58580-90) are claimed.  These can be used for recombinant
CC   production of the secreted proteins for analysis, characterisation,
CC   diagnostic or therapeutic use.  They can also be used as tissue or
CC   mol.wt. markers, for chromosome identification, to identify genetic
CC   disorders, to isolate new related DNA, as sources of primers for
CC   PCR, to generate antibodies, and in interaction trap assays.  The
CC   secreted proteins may also have many biological activities, e.g.
CC   cytokine, immunomodulator, haematopoiesis regulating activity,
```

```
CC   tissue growth activity, activin or inhibin activity, chemotactic or
CC   chemokinetic activity, haemostatic and thrombolytic activity,
CC   receptor/ligand activity, antiinflammatory, cadherin and tumour
CC   invasion suppressor activity, and tumour inhibition activity.  The
CC   proteins can be expressed in vivo from DNA, introduced in gene
CC   therapy vectors.
XX
SQ   Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 other;


alignment_scores:
            Quality:  905.50              Length:    474
              Ratio:  3.166                Gaps:     12
 Percent Similarity:  60.338   Percent Identity: 48.101

alignment_block:
 US-09-544-776-2 x V30920   ..

 Align seg 1/1  to: V30920  from: 1  to: 2386

       5 AspGlnSerProLeuValSerSerSerAspSerProProArgProGlnPr 21
         |||:::|||   ||||||:::::|||:::         :::|||
     654 GATCATTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGA 703

      21 oAlaPheLysTyrGlnPheValArgGluProGluAspGluGluGluGlu. 37
           |||:::  :::  :::  :::     :::::::::::::|||
     704 CTTATTTAGTGATGATTCAATACCTGACGTTCCACAAAAACAAGATGAAA 753

      38 .............GluGluGluGluGluGluAspGluAspGluAspLeu 49
                     :::|||:::      |||   :::   |||::::::
     754 CTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCATTTGAGTCAATG 803

      50 GluGluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerAlaAl 66
         |||  |||      |||:::              |||||||||
     804 ATAGAATATGAAAATAAGGAAAAA..............CTCAGTGCTTT 838

      66 aProValProThrAlaProAlaAlaGlyAlaProLeuMetAsp....... 80
          |||           |||   :::|||   |||   ::::::
     839 GCCA............CCTGAGGGAGGAAAGCCATATTTGGAATCTTTTA 876

      80 .................................................. 80

     877 AGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGATGAAGTTTCA 926

      80 .................................................. 80

     927 ACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTAC 976

      81 .......PheGlyAsnAsp.............................. 84
               ::::::||||||
     977 TGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAA 1026

      85 .............PheValProProAlaProArgGlyPheLeuProAla 96
                     |||         :::|||      ::::::
    1027 GAGAAACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAG 1076

      97 AlaProProValAlaProGluArgGlnProSerTrp.............. 108
         |||   :::      ::::::      |||:::
    1077 TTCCCTACATTGATCAGTTCTAAAACTGATTCATTTTCTAAATTAGCCAG 1126

     109 ................AspProSerProValSerSerThrValProAlaP 120
                        :::   |||      |||:::   :::   ||||
    1127 GGAATATACTGACCTAGAAGTATCCCACAAAAGTGAAATTGCTAATGCCC 1176

     120 roSerPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAsp 136
         ||:::      :::|||:::::::::      ::::::||||||:::|||
    1177 CGGAT......GGAGCTGGGTCATTGCCTTGCACAGAATTGCCCCATGAC 1220

     137 ..............AspGluProProAlaArgProPro............ 144
                       :::|||   ::::::
    1221 CTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTC 1270

     145 ...............................................P 145
```

```
                                                                |
    1271 AGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGC 1320

     145 roProProProAlaSerValSerProGlnAla......GluProValTrp 159
         |||||      ::::::::::::   ||||||      |||   :::
    1321 CTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTT 1370

     160 ThrProProAlaProAlaProAlaAlaProProSerThrProAlaAlaPr 176
           |||   :::   :::      |||      :::   |||:::
    1371 AAACCCAAAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATAC 1420

     176 oLysArgArgGlySerSerGlySerVal..................... 185
          :::::::::      |||   |||:::
    1421 AGAAAAAGAGGACAGATCACCATCTGCTATATTTTCAGCAGAGCTGAGTA 1470

     186 ........ValValAspLeuLeuTyrTrpArgAspIleLysLysThrGly 199
                 ||||||||||||||||||||||||||||||||||||||||||
    1471 AAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGA 1520

     200 ValValPheGlyAlaSerLeuPheLeuLeuLeuSerLeuThrValPheSe 216
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1521 GTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAG 1570

     216 rIleValSerValThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrI 233
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1571 CATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCA 1620

     233 leSerProArgIleTyrLysGlyValIleGlnAlaIleGlnLysSerAsp 249
         |||||   ||||||||||||||||||||||||||||||||||||||||||
    1621 TCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGAT 1670

     250 GluGlyHisProPheArgAlaTyrLeuGluSerGluValAlaIleSerGl 266
         ||||||||||||||||||               ||||||||||||||||||
    1671 GAAGGCCACCCATTCAGG..............GAAGTTGCTATATCTGA 1705

     266 uGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyHisValAsnCysT 283
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1706 GGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCA 1755

     283 hrIleLysGluLeuArgArgLeuPheLeuValAspAspLeuValAspSer 299
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1756 CGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCT 1805

     300 LeuLysPheAlaValLeuMetTrpValPheThrTyrValGlyAlaLeuPh 316
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1806 CTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTT 1855

     316 eAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerLeuPheSerValP 333
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1856 TAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTC 1905

     333 roValIleTyrGluArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeu 349
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1906 CTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTT 1955

     350 AlaAsnLysAsnValLysAspAlaMetAlaLysIleGlnAlaLysIlePr 366
         ||||||||||||||||||||||||||||||||||||||||||||||||||
    1956 GCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCC 2005

     366 oGlyLeuLysArgLysAlaGlu 373
         |||||||||||||||||||
    2006 TGGATTGAAGCGCAAAGCTGAA 2027

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:X75770

seq_documentation_block:
ID   X75770 standard; DNA; 3202 BP.
XX
AC   X75770;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Human neuroendocrine-specific protein NSP-A DNA.
```

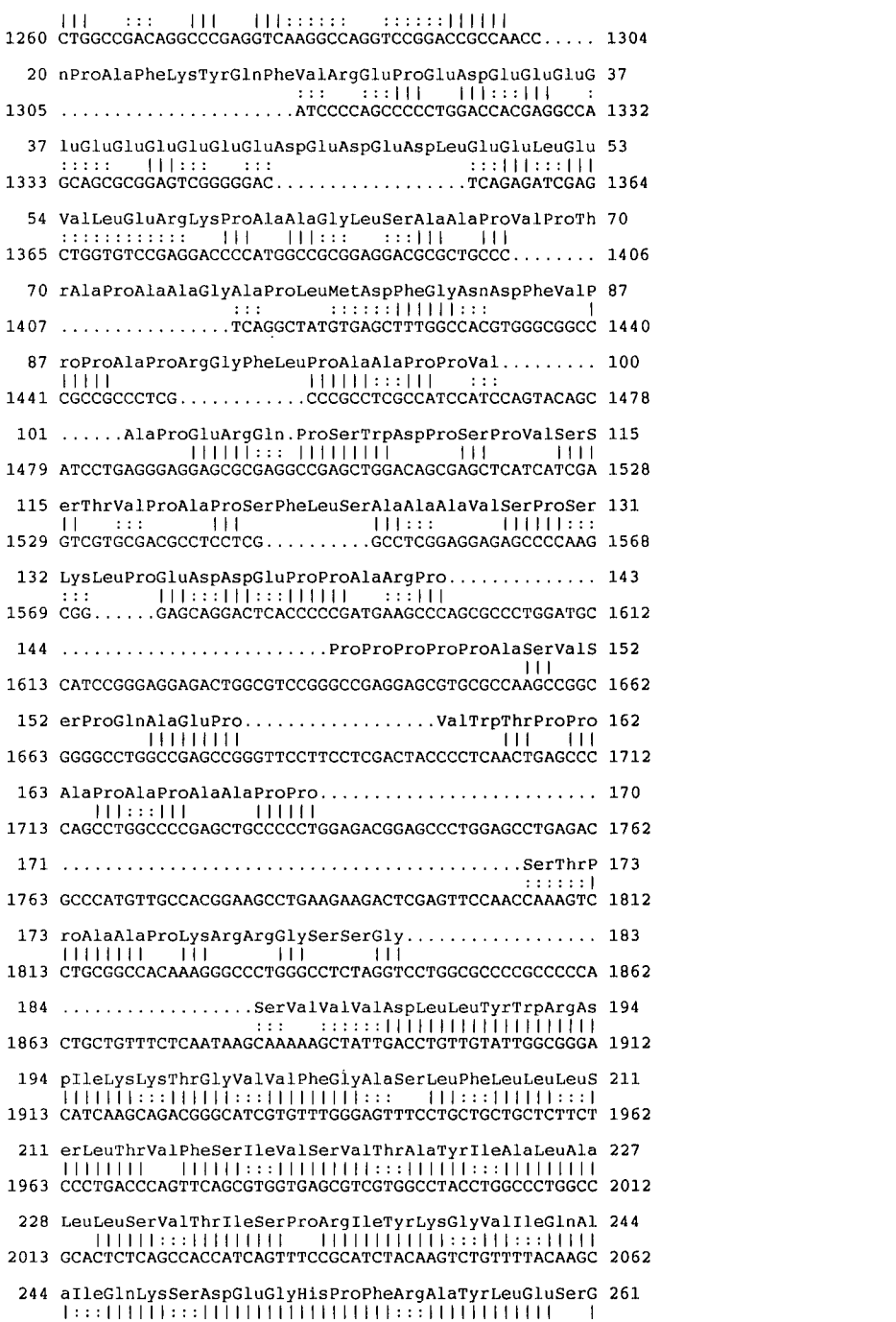
```
XX
KW   Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW   frameshift mutation; age-related disease; neurodegenerative disorder;
KW   Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW   Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW   diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW   ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW   neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
KW   glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW   bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW   high mobility group protein-C; neuroendocrine specific protein A; ss.
XX
OS   Homo sapiens.
XX
PN   WO9845322-A2.
XX
PD   15-OCT-1998.
XX
PF   02-APR-1998;   98WO-IB00705.
XX
PR   10-APR-1997;   97US-0043163.
XX
PA   (UYUT-) RIJKSUNIV UTRECHT.
PA   (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
PA   (UYRO-) UNIV ROTTERDAM ERASMUS.
XX
PI   Burbach JPH,  Grosveld FG,  Van Leeuwen FW;
XX
DR   WPI; 1998-609901/51.
XX
PT   Diagnosing disease by detecting frameshift mutations in RNA or
PT   corresponding protein mutations - used to diagnose cancer and
PT   neurological diseases, particularly Alzheimer's disease, and also
PT   for treatment and prevention with specific ribozymes or wild-type
PT   RNA
XX
PS   Disclosure; Figure 19; 258pp; English.
XX
CC   This invention describes a novel method for the diagnosis of a disease
CC   caused by, or associated with, an RNA molecule that has a frameshift
CC   mutation. The method is used to diagnose age-related diseases, especially
CC   cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
CC   disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
CC   multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
CC   and many others listed) or susceptibility to these disorders. The method
CC   allows a definitive diagnosis of Alzheimer's disease in living patients,
CC   at an early stage. It is based on the observation that disease may be
CC   caused by mutations in RNA rather than DNA. The invention describes the
CC   used of neuronal system RNA molecules, specifically proteins including
CC   beta-amyloid precursor protein (beta-APP), the microtubule associated
CC   proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
CC   associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
CC   neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
CC   protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
CC   2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
CC   protein-C (HMGP-C) and neuroendocrine specific protein A. This sequence
CC   encodes the wild type and mutant protein fragments represented in
CC   Y21434-Y21520.
XX
SQ   Sequence 3202 BP; 784 A; 891 C; 825 G; 702 T; 0 other;


alignment_scores:
            Quality:  747.50              Length:    430
              Ratio:  2.821                Gaps:     12
 Percent Similarity:  61.628   Percent Identity: 42.326

alignment_block:
 US-09-544-776-2 x X75770   ..

 Align seg 1/1  to: X75770  from: 1  to: 3202

      4 LeuAspGlnSerProLeuValSerSerSerAspSerProProArgProGl 20
```



```
    2063 AGTGCAGAAAACCGACGAAGGCCACCCTTTCAAGGCCTACTTGGAGCTTG 2112

     261 luValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeu 277
         ||:::::::::|||:::|||   :::||||||||||:::::
    2113 AGATCACCCTTTCTCAGGAGCAGATTCAGAAGTACACGGACTGCCTGCAG 2162

     278 GlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAs 294
           :::||||||   |||:::|||||||||||||||||||||||||||::
    2163 TTCTACGTGAACAGCACACTTAAGGAACTGAGGAGGCTCTTCCTTGTCCA 2212

     294 pAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrT 311
         :||||||||||||||||||||||||||||||||||||||:::::|||||
    2213 GGACCTGGTGGATTCCTTAAAATTTGCAGTCCTGATGTGGCTCCTGACCT 2262

     311 yrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIle 327
         ||||||||||||||||||||||||||||||||||||:::::|||::::::
    2263 ACGTTGGCGCTCTCTTCAATGGCCTGACCCTGCTGCTCATGGCTGTGGTT 2312

     328 SerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAs 344
         |||:::|||::::::||||||:::|||   :::||||||||||||||||
    2313 TCAATGTTTACTCTACCTGTAGTGTATGTTAAGCACCAGGCACAGATTGA 2362

     344 pHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysI 361
         |:::||||||||||||::::::   :::::::::   ::::::|||||||
    2363 CCAATATCTGGGACTTGTGAGGACTCACATAAATGCTGTTGTGGCAAAGA 2412

     361 leGlnAlaLysIleProGlyLeuLysArgLysAlaGlu 373
         ||||||||||||||||||   ||||||   ||||||
    2413 TTCAGGCTAAAATCCCAGGCGCTAAGAGGCACGCTGAG 2450

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V59748

seq_documentation_block:
ID   V59748 standard; DNA; 1766 BP.
XX
AC   V59748;
XX
DT   19-JAN-1999  (first entry)
XX
DE   Human secreted protein gene 92 clone HAUBL57.
XX
KW   Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW   diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW   developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW   immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW   inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW   cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW   osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW   endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS   Homo sapiens.
XX
PN   WO9839448-A2.
XX
PD   11-SEP-1998.
XX
PF   06-MAR-1998;   98WO-US04493.
XX
PR   02-OCT-1997;   97US-0061060.
PR   07-MAR-1997;   97US-0038621.
PR   07-MAR-1997;   97US-0040161.
PR   07-MAR-1997;   97US-0040162.
PR   07-MAR-1997;   97US-0040163.
PR   07-MAR-1997;   97US-0040333.
PR   07-MAR-1997;   97US-0040334.
PR   07-MAR-1997;   97US-0040336.
PR   07-MAR-1997;   97US-0040626.
PR   11-APR-1997;   97US-0043311.
PR   11-APR-1997;   97US-0043312.
PR   11-APR-1997;   97US-0043313.
PR   11-APR-1997;   97US-0043314.
PR   11-APR-1997;   97US-0043568.
PR   11-APR-1997;   97US-0043569.
PR   11-APR-1997;   97US-0043576.
PR   11-APR-1997;   97US-0043578.
PR   11-APR-1997;   97US-0043580.
PR   11-APR-1997;   97US-0043669.
PR   11-APR-1997;   97US-0043670.
PR   11-APR-1997;   97US-0043671.
PR   11-APR-1997;   97US-0043672.
PR   11-APR-1997;   97US-0043674.
PR   23-MAY-1997;   97US-0047492.
PR   23-MAY-1997;   97US-0047500.
PR   23-MAY-1997;   97US-0047501.
PR   23-MAY-1997;   97US-0047502.
PR   23-MAY-1997;   97US-0047503.
PR   23-MAY-1997;   97US-0047581.
PR   23-MAY-1997;   97US-0047582.
PR   23-MAY-1997;   97US-0047583.
PR   23-MAY-1997;   97US-0047584.
PR   23-MAY-1997;   97US-0047585.
PR   23-MAY-1997;   97US-0047586.
PR   23-MAY-1997;   97US-0047587.
PR   23-MAY-1997;   97US-0047588.
PR   23-MAY-1997;   97US-0047589.
PR   23-MAY-1997;   97US-0047590.
PR   23-MAY-1997;   97US-0047592.
PR   23-MAY-1997;   97US-0047593.
PR   23-MAY-1997;   97US-0047594.
PR   23-MAY-1997;   97US-0047595.
PR   23-MAY-1997;   97US-0047596.
PR   23-MAY-1997;   97US-0047597.
PR   23-MAY-1997;   97US-0047598.
PR   23-MAY-1997;   97US-0047599.
PR   23-MAY-1997;   97US-0047600.
PR   23-MAY-1997;   97US-0047601.
PR   23-MAY-1997;   97US-0047612.
PR   23-MAY-1997;   97US-0047613.
PR   23-MAY-1997;   97US-0047614.
PR   23-MAY-1997;   97US-0047615.
PR   23-MAY-1997;   97US-0047617.
PR   23-MAY-1997;   97US-0047618.
PR   23-MAY-1997;   97US-0047632.
PR   23-MAY-1997;   97US-0047633.
PR   06-JUN-1997;   97US-0048964.
PR   06-JUN-1997;   97US-0048974.
PR   13-JUN-1997;   97US-0049610.
PR   08-JUL-1997;   97US-0051926.
PR   16-JUL-1997;   97US-0052874.
PR   18-AUG-1997;   97US-0055724.
PR   22-AUG-1997;   97US-0056630.
PR   22-AUG-1997;   97US-0056631.
PR   22-AUG-1997;   97US-0056632.
PR   22-AUG-1997;   97US-0056636.
PR   22-AUG-1997;   97US-0056637.
PR   22-AUG-1997;   97US-0056662.
PR   22-AUG-1997;   97US-0056664.
PR   22-AUG-1997;   97US-0056845.
PR   22-AUG-1997;   97US-0056862.
PR   22-AUG-1997;   97US-0056864.
PR   22-AUG-1997;   97US-0056872.
PR   22-AUG-1997;   97US-0056874.
PR   22-AUG-1997;   97US-0056875.
PR   22-AUG-1997;   97US-0056876.
PR   22-AUG-1997;   97US-0056877.
PR   22-AUG-1997;   97US-0056878.
PR   22-AUG-1997;   97US-0056879.
PR   22-AUG-1997;   97US-0056880.
PR   22-AUG-1997;   97US-0056881.
PR   22-AUG-1997;   97US-0056882.
PR   22-AUG-1997;   97US-0056884.
PR   22-AUG-1997;   97US-0056886.
PR   22-AUG-1997;   97US-0056887.
PR   22-AUG-1997;   97US-0056888.
PR   22-AUG-1997;   97US-0056889.
PR   22-AUG-1997;   97US-0056892.
```

```
PR   22-AUG-1997;   97US-0056893.
PR   22-AUG-1997;   97US-0056894.
PR   22-AUG-1997;   97US-0056903.
PR   22-AUG-1997;   97US-0056908.
PR   22-AUG-1997;   97US-0056909.
PR   22-AUG-1997;   97US-0056910.
PR   22-AUG-1997;   97US-0056911.
PR   05-SEP-1997;   97US-0057650.
PR   05-SEP-1997;   97US-0057669.
PR   05-SEP-1997;   97US-0057761.
PR   12-SEP-1997;   97US-0058785.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Bednarik DP,  Brewer LA,  Carter KC,  Duan R,  Ebner R,  Endress GA;
PI   Feng P,  Ferrie AM,  Fischer CL,  Florence KA,  Greene JM,  Hu JS;
PI   Kyaw H,  Lafleur DW,  Li Y,  Moore PA,  Ni J,  Olsen HS,  Rosen CA;
PI   Ruben SM,  Shi Y,  Soppet DR,  Young PE,  Yu GL,  Zeng Z;
XX
DR   WPI; 1998-506364/43.
DR   P-PSDB; W74963.
XX
PT   New isolated human genes and the secreted polypeptide(s) they encode
PT   - useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders
XX
PS   Claim 1; Page 473-474; 721pp; English.
XX
CC   This sequence represents a nucleic acid molecule designated Gene 92 from
CC   the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
CC   209043) which encodes a secreted human protein.  The gene can be used to
CC   generate fusion proteins by linking to the gene to a human immunoglobulin
CC   Fc portion (e.g. V59502) for increasing the stability of the fused
CC   protein as compared to the human protein only.
CC   The invention relates to 186 novel genes and their fragments (nucleic
CC   acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 186 polynucleotides, based on
CC   which tissues they are most highly expressed in (see V59511 for described
CC   uses).
XX
SQ   Sequence 1766 BP; 463 A; 437 C; 383 G; 481 T; 2 other;


alignment_scores:
            Quality:  672.50              Length:    348
              Ratio:  2.924                Gaps:      8
 Percent Similarity:  66.092   Percent Identity: 43.678

alignment_block:
 US-09-544-776-2 x V59748   ..

 Align seg 1/1  to: V59748  from: 1  to: 1766

      32 GluAspGluGluGluGluGluGluGluGluGluAspGluAspGluAs 48
         |||:::   |||:::::::|||:::   :::|||:::   |||   :::||
       6 GAATCGGCAGAGCGGCACGAGCGGCCACGAGAGCAGGCGGAGTAAAGGGA 55

      48 pLeuGluGluLeuGluValLeuGluArgLysProAlaAlaGlyLeuSerA 65
         ||||:::|||                  |||:::|||||||||
      56 CTTGAGCGAG.....................CCAGTTGCCGGATTATTCT 84

      65 laAlaProValProThrAlaProAlaAlaGlyAlaProLeuMetAspPhe 81
            |||
      85 ATTTCCCC..................................... 92

      82 GlyAsnAspPheValProProAlaProArgGlyPheLeuProAlaAlaPr 98
                 :::   |||||||||      |||   |||   :::
      93 .........TCCCTCTCTCCCGCCCCGTATCTCTTTTCACCCTTCTCCCA 133

      98 oPro............ValAlaProGluArgGlnProSerTrpAspProS 111
          |||            :::|||   :::|||:::|||           |
     134 CCCTCGCTCGCGTASCATGGCGGAGCGTCGGCGGCCACTC.........A 174

     111 erProValSerSerThrValProAlaProSerPheLeuSerAlaAlaAla 127
         |||||:::   |||
     175 GTCCCATTCCATCT..................................... 188

     128 ValSerProSerLysLeuProGluAspAspGluProProAlaArgProPr 144
                                            |||   ||||||
     189 .....................................CCTCGTCGTCCTTC 202

     144 oProProProProAlaSerValSerProGlnAlaGluProValTrpThrP 161
             |||                                       :::
     203 GGAGCCG.....................................AGCC 213

     161 roProAlaProAlaProAla..AlaProProSerThrProAlaAlaProL 177
         |||   ||||||   |||  :::|||   :::   ||||||
     214 GTCCGCGCCCGGCGGCGGCGGGAGCCCAGGAGCCTGCCCCGCCCTGGGGA 263

     177 ysArgArgGlySerSerGlySerValValValAspLeuLeuTyrTrpArg 193
           :::      ||||||:::   :::|||   ||||||:::::|||||
     264 CGAAGAGCTGCAGCTCCTCCTGTGCGGTGCACGATCTGATTTTCTGGAGA 313

     194 AspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLe 210
         |||:::||||||||||||   |||||||||:::::|||:::::|||||
     314 GATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACGCTGATCATGCTGCT 363

     210 uSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLeuA 227
         ||||||:::::||||||:::::||||||:::::|||:::   ||||
     364 TTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTCATCCTGG 413

     227 laLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleGln 243
         ||||||||||||||||||||||   ||||||||||:::||||||||||
     414 CTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAA 463

     244 AlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSe 260
         |||:::||||||||:::|||||||||||||||:::||||||||:::
     464 GCTGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGT 513

     260 rGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaL 277
          :::::::::::::|||:::|||      ::::::|||   |||:::|||:
     514 AGACATTACTCTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCA 563

     277 euGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuVal 293
         ::   |||:::|||   ::::::|||   :::   ||||||||||||||
     564 TGGTGCACATCAACAGGGCCCTGAAACTCATTATTCGTCTCTTTCTGGTA 613

     294 AspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPheTh 310
         :::|||||||||||||||||||:::||||||:::||||||:::||
     614 GAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTCATGTGGCTGATGAC 663

     310 rTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuI 327
         |||||||||||||:::||||||||:::||||||||||||||||||   :
     664 CTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTTGCTGAAC 713

     327 leSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnIle 343
         ::   :::|||||||||||||:::::|||||:::::::::::::||||||
     714 TGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 763

     344 AspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLy 360
         |||||||||:::|||:::|||:::   :::::|||:::   :::   ||
     764 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAA 813

     360 sIleGlnAlaLysIleProGlyLeu...LysArgLysAlaGlu 373
         ||||||||||||:::||||||:::   |||:::|||||||||
     814 GATCCAAGCAAAACTCCCTGGAATCGCCAAAAAAAAGGCAGAA 856

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1998.DAT:V59749

seq_documentation_block:
ID   V59749 standard; DNA; 2664 BP.
XX
```

AC V59749;
XX
DT 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 92 clone HAUBL57.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057669.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
DR WPI; 1998-506364/43.
DR P-PSDB; W74964.
XX
PT New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 475-476; 721pp; English.
XX
CC This sequence represents a nucleic acid molecule designated Gene 92 from
CC the human cDNA clone HAUBL57 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. V59502) for increasing the stability of the fused
CC protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic

```
CC   acid sequences: V59511-V59812; amino acid sequences W74731-W75026) which
CC   are useful for preventing, treating or ameliorating  medical conditions
CC   e.g. by protein or gene therapy.  Also, pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new polynucleotides.
CC   Specific uses are described for each of the 186 polynucleotides, based on
CC   which tissues they are most highly expressed in (see V59511 for described
CC   uses).
XX
SQ   Sequence 2664 BP; 707 A; 605 C; 566 G; 779 T; 7 other;


alignment_scores:
           Quality:  659.50              Length:    338
             Ratio:  2.971                 Gaps:      8
 Percent Similarity:  65.680   Percent Identity: 44.083

alignment_block:
 US-09-544-776-2 x V59749   ..

 Align seg 1/1  to: V59749  from: 1  to: 2664

      42 GluGluAspGluAspGluAspLeuGluGluLeuGluValLeuGluArgLy 58
         |||:::   |||   :::||||||:::|||
      11 GAGCAGGCGGAGTAAAGGGACTTGAGCGAG..................... 40

      58 sProAlaAlaGlyLeuSerAlaAlaProValProThrAlaProAlaAlaG 75
          |||:::|||||||||          |||
      41 .CCAGTTGCCGGATTATTCTATTTCCCC..................... 67

      75 lyAlaProLeuMetAspPheGlyAsnAspPheValProProAlaProArg 91
                                                :::   ||||||||
      68 ............................TCCCTCTCTCCCGCCCCGTAT 88

      92 GlyPheLeuProAlaAlaProPro.............ValAlaProGluAr 104
            |||   |||   :::   |||             :::|||   :::||
      89 CTCTTTTCACCCTTCTCCCACCCTCGCTCGCGTASCATGGCGGAGCGTCG 138

     104 gGlnProSerTrpAspProSerProValSerSerThrValProAlaProS 121
         |:::|||             ||||||:::   |||
     139 GCGGCCACTC.........AGTCCCATTCCATCT................. 163

     121 erPheLeuSerAlaAlaAlaValSerProSerLysLeuProGluAspAsp 137

     163 ..................................................... 163

     138 GluProProAlaArgProProProProProProAlaSerValSerProGl 154
               |||   ||||||      |||
     164 ......CCTCGTCGTCCTTCGGAGCCG.......................... 184

     154 nAlaGluProValTrpThrProProAlaProAlaProAla..AlaProPr 170
                         :::   |||   ||||||   |||  :::|||
     185 ................AGCCGTCCGCGCCCGGCGGCGGCGGGAGCCCAGG 218

     170 oSerThrProAlaAlaProLysArgArgGlySerSerGlySerValValV 187
          :::   ||||||      :::      ||||||:::   :::|||
     219 AGCCTGCCCCGCCCTGGGGACGAAGAGCTGCAGCTCCTCCTGTGCGGTGC 268

     187 alAspLeuLeuTyrTrpArgAspIleLysLysThrGlyValValPheGly 203
           ||||||:::::|||||||||:::||||||||||||   |||||||||
     269 ACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGC 318

     204 AlaSerLeuPheLeuLeuLeuSerLeuThrValPheSerIleValSerVa 220
         ::::::|||::::::|||||||||||:::::::||||||::::::|||||
     319 ACCACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGT 368

     220 lThrAlaTyrIleAlaLeuAlaLeuLeuSerValThrIleSerProArgI 237
         |::::::|||:::   |||||||||||||||||||||||||   ||||
     369 GGTTTCTTACCTCATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGA 418

     237 leTyrLysGlyValIleGlnAlaIleGlnLysSerAspGluGlyHisPro 253
         ||||||||:::|||||||||||||:::||||||||||:::||||||||||||
     419 TCTACAAGTCCGTCATCCAAGCTGTACAGAAGTCAGAAGAAGGCCATCCA 468

     254 PheArgAlaTyrLeuGluSerGluValAlaIleSerGluGluLeuValGl 270
         |||:::|||||||||:::   :::::::::::|||:::|||      ::
     469 TTCAAAGCCTACCTGGACGTAGACATTACTCTGTCCTCAGAAGCTTTCCA 518

     270 nLysTyrSerAsnSerAlaLeuGlyHisValAsnCysThrIleLysGluL 287
         ::::|||   |||:::|||:::   |||:::|||   ::::::|||   :
     519 TAATTACATGAATGCTGCCATGGTGCACATCAACAGGGCCCTGAAACTCA 568

     287 euArgArgLeuPheLeuValAspAspLeuValAspSerLeuLysPheAla 303
         ::   ||||||||||||||:::|||||||||||||||||||||:::|||
     569 TTATTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 618

     304 ValLeuMetTrpValPheThrTyrValGlyAlaLeuPheAsnGlyLeuTh 320
         |||:::||||||:::::|||||||||||||||:::||||||||||:::||
     619 GTCTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCAC 668

     320 rLeuLeuIleLeuAlaLeuIleSerLeuPheSerValProValIleTyrG 337
         ||||||||||||||||   :::   :::|||||||||||||:::::::|||
     669 CCTTCTAATTCTTGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATG 718

     337 luArgHisGlnAlaGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsn 353
         ||:::::::::::|||||||||||||||:::|||:::|||:::   :::
     719 AGAAGTACAAGACCCAGATTGATCACTATGTTGGCATCGCCCGAGATCAG 768

     354 ValLysAspAlaMetAlaLysIleGlnAlaLysIleProGlyLeu...Ly 369
         :::|||:::   :::   |||||||||||||||:::|||||||:::-  ||
     769 ACCAAGTCAATTGTTGAAAAGATCCAAGCAAAACTCCCTGGAATCGCCAA 818

     369 sArgLysAlaGlu 373
         |:::|||||||||
     819 AAAAAAGGCAGAA 831

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z36240

seq_documentation_block:
ID   Z36240 standard; cDNA; 1668 BP.
XX
AC   Z36240;
XX
DT   22-FEB-2000  (first entry)
XX
DE   cDNA encoding a bone marrow secreted protein designated BMS240.
XX
KW   Bone marrow secreted protein; bone marrow stromal cell; cytokine;
KW   cell proliferation; cell differentiation; hematopoiesis; anaemia;
KW   myeloid cell deficiency; lymphoid cell deficiency; myeloid cell;
KW   erythroid progenitor cell; colony stimulating factor; granulocyte;
KW   monocyte; macrophage; myelo-suppression; megakaryocyte; platelet;
KW   platelet disorder; thrombocytopenia; hematopoeitic stem cell;
KW   stem cell disorder; aplastic anaemia; bone differentiation;
KW   paroxysmal nocturnal hemoglobinuria; bone growth; cartilage; tendon;
KW   ligament; nerve; wound healing; tissue repair; burn; incision; ulcer;
KW   bone fracture; cartilage damage; artificial joint; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             99..809
FT                   /*tag=  a
FT                   /product= "bone marrow secreted protein"
FT   polyA_signal    1626..1631
FT                   /*tag=  b
XX
PN   WO9933979-A2.
XX
PD   08-JUL-1999.
XX
PF   18-DEC-1998;   98WO-US27008.
XX
PR   30-DEC-1997;   97US-0068958.
PR   24-SEP-1998;   98US-0101603.
PR   30-SEP-1998;   98US-0102540.
```

```
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Lin H,  Cao L;
XX
DR   WPI; 2000-038344/03.
DR   P-PSDB; Y53634.
XX
PT   New isolated human polynucleotide and secreted proteins can induce
PT   production of other cytokines in certain cell populations -
XX
PS   Claim 11; Page 98-100; 120pp; English.
XX
CC   Z36228-49 encode bone marrow secreted proteins of human bone marrow
CC   stromal cells. The proteins can exhibit cytokine, cell proliferation, or
CC   cell differentiation activity (either inducing or inhibiting). They can
CC   be used to support colony forming cells or factor-dependent cell lines,
CC   to regulate hematopoiesis, and to treat myeloid or lymphoid cell
CC   deficiencies. In addition, they may be used to support the growth and
CC   proliferation of erythroid progenitor cells, and to treat various
CC   anaemias. They can have colony stimulating factor (CSF) activity and can
CC   be used to support the growth and proliferation of myeloid cells such as
CC   granulocytes, monocytes or macrophages, to prevent or treat
CC   myelo-suppression, to support the growth and proliferation of
CC   megakaryocytes and platelets, thereby allowing prevention or treatment
CC   of platelet disorders such as thrombocytopenia, to support the growth
CC   and proliferation of hematopoeitic stem cells, either in place of or in
CC   conjunction with platelet transfusions, to treat stem cell disorders,
CC   such as aplastic anaemia and paroxysmal nocturnal hemoglobinuria, or to
CC   repopulate the stem cell compartment after irradiation or chemotherapy.
CC   They can be used for growth or differentiation of bone, cartilage,
CC   tendon, ligament, or nerve tissue, as well as for wound healing and
CC   tissue repair and replacement, and in the treatment of burns, incisions
CC   and ulcers, to induce cartilage and/or bone growth in circumstances where
CC   bone is not normally formed and thus have an application in healing bone
CC   fractures and cartilage damage or defects, prophylactic use in fracture
CC   reduction and also in the improved fixation of artificial joints.
XX
SQ   Sequence 1668 BP; 435 A; 414 C; 349 G; 470 T; 0 other;


alignment_scores:
            Quality:  655.00              Length:    265
              Ratio:  3.180                 Gaps:      5
 Percent Similarity:  77.736   Percent Identity: 50.566

alignment_block:
 US-09-544-776-2 x Z36240   ..

 Align seg 1/1  to: Z36240  from: 1  to: 1668

     131 SerLysLeuProGlu...AspAspGluProProAlaArgProPro..... 144
         |||:::||||||:::   :::   :::||||||:::   ||||||
      12 AGCCAGTTGCCGGATTATTCTATTTCCCCTCCCTCTCTCCCGCCCCGTAT 61

     145 .........ProProProProAlaSerValSerProGlnAlaGluProV 158
                 |||   |||      :::         :::|||||||||
      62 CTCTTTTCACCCTTCTCCCACCCTCGCTCGCGTAGCCATGGCGGAGCCGT 111

     158 alTrpThr..................................... 160
             :::
     112 CGGCGGCCACTCAGTCCCATTCCATCTCCTCGTCGTCCTTCGGAGCCGAG 161

     161 ProProAlaPro...AlaProAlaAlaProProSerThrProAlaAlaPr 176
         |||   ||||||   :::   :::::::|||   :::   ||||||
     162 CCGTCCGCGCCCGGCGGCGGCGGGAGCCCAGGAGCCTGCCCCGCCCTGGG 211

     176 oLysArgArgGlySerSerGlySerValValValAspLeuLeuTyrTrpA 193
             :::      ||||||:::   :::|||   ||||||::::::||||
     212 GACGAAGAGCTGCAGCTCCTCCTGTGCGGTGCACGATCTGATTTTCTGGA 261

     193 rgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 209
         |||||:::|||||||||||||   |||||||||:::::::|||:::::|||

     262 GAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACGCTGATCATGCTG 311

     210 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe 226
         |||||||||:::::|||||:::::::|||||:::::|||:::   ||
     312 CTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTCATCCT 361

     226 uAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleG 243
         |||||||||||||||||||||||||   ||||||||||||:::|||||||
     362 GGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCC 411

     243 lnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 259
         |||||:::|||||||||:::|||||||||||||||:::||||||||||:::
     412 AAGCTGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGAC 461

     260 SerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAl 276
             :::::::::::|||:::|||      ::::::|||   |||:::||
     462 GTAGACATTACTCTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGC 511

     276 aLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuV 293
         |:::   |||:::|||   ::::::|||   :::   ||||||||||||
     512 CATGGTGCACATCAACAGGGCCCTGAAACTCATTATTCGTCTCTTTCTGG 561

     293 alAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 309
         ||:::|||||||||||||||||||:::||||||:::||||||::::::
     562 TAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTCATGTGGCTGATG 611

     310 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLe 326
         ||||||||||||||:::|||||||||:::|||||||||||||||||||
     612 ACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTTGCTGA 661

     326 uIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnI 343
          :::   :::||||||||||||:::::::||||||:::::::::::||||
     662 ACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGA 711

     343 leAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 359
         ||||||||||:::|||:::|||:::   ::::::|||:::   :::
     712 TTGATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAA 761

     360 LysIleGlnAlaLysIleProGlyLeu...LysArgLysAlaGlu 373
         ||||||||||||||:::||||||:::   |||:::|||||||||
     762 AAGATCCAAGCAAAACTCCCTGGAATCGCCAAAAAAAAGGCAGAA 806

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z38319

seq_documentation_block:
ID   Z38319 standard; cDNA; 1759 BP.
XX
AC   Z38319;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Human transmembrane protein cDNA clone HP02061.
XX
KW   HP02061; transmembrane domain; Saos-2; homology;
KW   neuroendocrine-specific protein C; antibody; assay reagent;
KW   diagnostic marker; primer; probe; antisense; gene therapy;
KW   agonist; antagonist; ligand; therapeutic; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             142..852
FT                   /*tag=  a
FT                   /product␣ "Human transmembrane protein HP02061"
XX
PN   WO9955862-A2.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-JP02226.
XX
PR   28-APR-1998;   98JP-0119395.
XX
```

```
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2000-023358/02.
DR   P-PSDB; Y52387.
XX
PT   Human proteins with transmembrane domains, involved in control of cell
PT   proliferation and differentiation, useful for treating e.g. cancer or
PT   inflammation  -
XX
PS   Claim 4; Page 92-94; 114pp; English.
XX
CC   This sequence represents the human cDNA clone HP02061
CC   which encodes a 26 kD protein with two putative transmembrane
CC   domains. The cDNA was isolated from a Saos-2 (human osteosarcoma cell
CC   line) cDNA library. The protein has homology with the human
CC   neuroendocrine-specific protein C (PIR Accession No. I60904),
CC   and may have a similar function. The protein may be used
CC   to raise specific antibodies, as assay reagents, as
CC   diagnostic tissue markers, for the isolation of cognate receptors,
CC   ligands and binding proteins, and as biologically active agents.
CC   Nucleotides encoding the protein may be used as primers and probes or
CC   antisense molecules, and in gene therapy. Cells transformed with these
CC   nucleotides may be used to screen for agonists and antagonists which are
CC   potentially useful therapeutically.
XX
SQ   Sequence 1759 BP; 454 A; 433 C; 376 G; 496 T; 0 other;


alignment_scores:
            Quality:  655.00              Length:    265
              Ratio:  3.180                Gaps:      5
 Percent Similarity:  77.736   Percent Identity: 50.566

alignment_block:
 US-09-544-776-2 x Z38319   ..

 Align seg 1/1  to: Z38319  from: 1  to: 1759

     131 SerLysLeuProGlu...AspAspGluProProAlaArgProPro..... 144
         |||:::||||||:::   :::   :::|||||||:::   ||||||
      55 AGCCAGTTGCCGGATTATTCTATTTCCCCTCCCTCTCTCCCGCCCCGTAT 104

     145 .........ProProProProAlaSerValSerProGlnAlaGluProV 158
                   |||   |||      :::         :::|||||||||
     105 CTCTTTTCACCCTTCTCCCACCCTCGCTCGCGTAGCCATGGCGGAGCCGT 154

     158 alTrpThr..................................... 160
             :::
     155 CGGCGGCCACTCAGTCCCATTCCATCTCCTCGTCGTCCTTCGGAGCCGAG 204

     161 ProProAlaPro...AlaProAlaAlaProProSerThrProAlaAlaPr 176
         |||   ||||||   :::   :::::::|||   :::   ||||||
     205 CCGTCCGCGCCCGGCGGCGGCGGGAGCCCAGGAGCCTGCCCCGCCCTGGG 254

     176 oLysArgArgGlySerSerGlySerValValValAspLeuLeuTyrTrpA 193
           :::       ||||||:::   :::|||   ||||||::::::|||
     255 GACGAAGAGCTGCAGCTCCTCCTGTGCGGTGCACGATCTGATTTTCTGGA 304

     193 rgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeu 209
         |||||:::||||||||||||   |||||||||:::::|||:::::|||
     305 GAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACGCTGATCATGCTG 354

     210 LeuSerLeuThrValPheSerIleValSerValThrAlaTyrIleAlaLe 226
         |||||||||:::::|||||:::::|||||:::::|||:::   ||
     355 CTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTCATCCT 404

     226 uAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyValIleG 243
         |||||||||||||||||||||||   ||||||||||||:::|||||||
     405 GGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCC 454

     243 lnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGlu 259
         |||||:::|||||||||:::|||||||||||||||:::|||||||||:::
     455 AAGCTGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGAC 504

     260 SerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAl 276
           :::::::::::::|||:::|||      :::::::|||   |||:::||
     505 GTAGACATTACTCTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGC 554

     276 aLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuPheLeuV 293
         |:::   |||:::|||   :::::::|||   :::   ||||||||||||
     555 CATGGTGCACATCAACAGGGCCCTGAAACTCATTATTCGTCTCTTTCTGG 604

     293 alAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrpValPhe 309
         ||:::|||||||||||||||||||:::||||||:::||||||::::::
     605 TAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTCATGTGGCTGATG 654

     310 ThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLe 326
         ||||||||||||||||:::|||||||||:::||||||||||||||||||
     655 ACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTTGCTGA 704

     326 uIleSerLeuPheSerValProValIleTyrGluArgHisGlnAlaGlnI 343
          :::   :::||||||||||||:::::|||||:::::::::::::||||
     705 ACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGA 754

     343 leAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAla 359
         ||||||||||:::|||:::|||:::   :::::::|||:::   :::
     755 TTGATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAA 804

     360 LysIleGlnAlaLysIleProGlyLeu...LysArgLysAlaGlu 373
         ||||||||||||||:::||||||:::   |||:::||||||||
     805 AAGATCCAAGCAAAACTCCCTGGAATCGCCAAAAAAAAGGCAGAA 849

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA1999.DAT:X60810

seq_documentation_block:
ID   X60810 standard; DNA; 1656 BP.
XX
AC   X60810;
XX
DT   09-AUG-1999  (first entry)
XX
DE   Human secreted protein encoding DNA (clone yb8-1).
XX
KW   Secreted protein; kidney; lung; brain; blood; testis; bone marrow;
KW   nutritional activity; cytokine; cell proliferation; immune stimulation;
KW   hematopoiesis regulation; tissue growth; thrombolytic; gene therapy;
KW   anti-inflammatory; tumour invasion; ss.
XX
OS   Homo sapiens.
XX
PN   WO9926961-A1.
XX
PD   03-JUN-1999.
XX
PF   24-NOV-1998;   98WO-US25149.
XX
PR   23-NOV-1998;   98US-0197886.
PR   26-NOV-1997;   97US-0066804.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Clark HF,  Collins-Racie LA,  Evans C;
PI   Fechtel K,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Steininger RJ,  Treacy M,  Wong GG;
XX
DR   WPI; 1999-357809/30.
DR   P-PSDB; Y17228.
XX
PT   New polynucleotides encoding secreted proteins
XX
PS   Claim 39; Page 125-126; 133pp; English.
XX
CC   The invention relates to secreted proteins (Y17219-228) encoded by
```

```
CC   polynucleotides obtained from human fetal kidney, adult lung, adult
CC   kidney, adult brain, adult blood, adult testes, and fetal brain and
CC   murine adult bone marrow cDNA libraries. The secretd protein nucleic acid
CC   sequences (X6801-811) correspond to clones bd306-7, gj283-6, fk317-3,
CC   k213-2x, na316-1, nf93-20, np164-1, pe204-1, ya1-1 and yb-1, (all clones
CC   are deposited as ATCC 98599); The PNs and proteins are predicted to have
CC   biological activities which would make them suitable for treating,
CC   preventing or ameliorating medical conditions in humans and animals,
CC   although no supporting data is given. Suggested activities include
CC   nutritional activity, cytokine and cell proliferation/differentiation
CC   activity, immune stimulating (e.g. as vaccines) or suppressing activity,
CC   hematopoiesis regulating activity, tissue growth activity, activin/
CC   inhibin activity, chemotactic/chemokinetic activity, haemostatic and
CC   thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC   activity, cadherin/tumour invasion suppressor activity, and tumour
CC   inhibition activity. The PNs are also stated to be useful for gene
CC   therapy.
XX
SQ   Sequence 1656 BP; 473 A; 389 C; 340 G; 454 T; 0 other;


alignment_scores:
            Quality:  644.50              Length:    246
              Ratio:  3.255                 Gaps:      5
 Percent Similarity:  80.488   Percent Identity: 53.659

alignment_block:
 US-09-544-776-2 x X60810   ..

 Align seg 1/1  to: X60810  from: 1  to: 1656

     139 ProProAla.....................ArgProProProPr 146
         ||||||:::                     ||||||      ||
       7 CCACCCTCGCTCGCGTAGCCATGGCGGAGCCGTCGGCGGCCACTCAGTCC 56

     146 oProProAlaSerValSerProGlnAlaGluProValTrpThrProProA 163
         |   |||:::         |||   :::||||||      :::   |||
      57 CATTCCATCTCCTCGTCGTCCT...TCGGAGCCG......AGCCGTCCGC 97

     163 laProAlaProAla..AlaProProSerThrProAlaAlaProLysArgA 179
           ||||||   |||  :::|||   :::   ||||||        :::
      98 GCCCGGCGGCGGCGGGAGCCCAGGAGCCTGCCCCGCCCTGGGGACGAAGA 147

     179 rgGlySerSerGlySerValValValAspLeuLeuTyrTrpArgAspIle 195
           ||||||:::   :::|||   ||||||::::::|||||||||:::
     148 GCTGCAGCTCCTCCTGTGCGGTGCACGATCTGATTTTCTGGAGAGATGTG 197

     196 LysLysThrGlyValValPheGlyAlaSerLeuPheLeuLeuLeuSerLe 212
         ||||||||||   |||||||||::::::|||::::::|||||||||||
     198 AAGAAGACTGGGTTTGTCTTTGGCACCACGCTGATCATGCTGCTTTCCCT 247

     212 uThrValPheSerIleValSerValThrAlaTyrIleAlaLeuAlaLeuL 229
         |::::::||||||::::::||||||::::::|||:::   ||||||||||
     248 GGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCTCATCCTGGCTCTTC 297

     229 euSerValThrIleSerProArgIleTyrLysGlyValIleGlnAlaIle 245
         ||||||||||||||||   ||||||||||||:::||||||||||||:::
     298 TCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGCTGTA 347

     246 GlnLysSerAspGluGlyHisProPheArgAlaTyrLeuGluSerGluVa 262
         |||||||||:::|||||||||||||||:::||||||||:::   :::::
     348 CAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACAT 397

     262 lAlaIleSerGluGluLeuValGlnLysTyrSerAsnSerAlaLeuGlyH 279
         :::::::|||:::|||      ::::::|||   |||:::|||:::   |
     398 TACTCTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGC 447

     279 isValAsnCysThrIleLysGluLeuArgArgLeuPheLeuValAspAsp 295
         ||:::|||   ::::::|||   :::   ||||||||||||||:::|||
     448 ACATCAACAGGGCCCTGAAACTCATTATTCGTCTCTTTCTGGTAGAAGAT 497

     296 LeuValAspSerLeuLysPheAlaValLeuMetTrpValPheThrTyrVa 312
         ||||||||||||||||||:::|||||||:::||||||::::::||||||||
```

```
     498 CTGGTTGACTCCTTGAAGCTGGCTGTCTTCATGTGGCTGATGACCTATGT 547

     312 lGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLeuAlaLeuIleSerL 329
         |||||||:::||||||||:::||||||||||||||||   :::   :
     548 TGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCTTGCTGAACTGCTCA 597

     329 euPheSerValProValIleTyrGluArgHisGlnAlaGlnIleAspHis 345
         ::||||||||||||:::::::||||||:::::::::::::||||||||||
     598 TTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGATCAC 647

     346 TyrLeuGlyLeuAlaAsnLysAsnValLysAspAlaMetAlaLysIleGl 362
         |||:::|||:::|||:::   :::::::|||:::   :::   ||||||||
     648 TATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCA 697

     362 nAlaLysIleProGlyLeu...LysArgLysAlaGlu 373
         |||||||:::||||||:::   |||:::|||||||||
     698 AGCAAAACTCCCTGGAATCGCCAAAAAAAAGGCAGAA 734

seq_name: /SIDS6/gcgdata/geneseq/geneseqn/NA2000.DAT:Z38318

seq_documentation_block:
ID   Z38318 standard; cDNA; 708 BP.
XX
AC   Z38318;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Human transmembrane protein cDNA clone HP02061 coding sequence.
XX
KW   HP02061; transmembrane domain; Saos-2; homology;
KW   neuroendocrine-specific protein C; antibody; assay reagent;
KW   diagnostic marker; primer; probe; antisense; gene therapy;
KW   agonist; antagonist; ligand; therapeutic; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..708
FT                   /*tag= a
FT                   /product= "Human transmembrane protein HP02061"
FT                   /note= "No stop codon given in the specification"
XX
PN   WO9955862-A2.
XX
PD   04-NOV-1999.
XX
PF   27-APR-1999;   99WO-JP02226.
XX
PR   28-APR-1998;   98JP-0119395.
XX
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2000-023358/02.
DR   P-PSDB; Y52387.
XX
PT   Human proteins with transmembrane domains, involved in control of cell
PT   proliferation and differentiation, useful for treating e.g. cancer or
PT   inflammation  -
XX
PS   Claim 3; Page 85; 114pp; English.
XX
CC   This sequence represents the coding sequence of human cDNA clone
CC   HP02061 which encodes a 26 kD protein with two putative transmembrane
CC   domains. The cDNA was isolated from a Saos-2 (human osteosarcoma cell
CC   line) cDNA library. The protein has homology with the human
CC   neuroendocrine-specific protein C (PIR Accession No. I60904),
CC   and may have a similar function. The protein may be used
CC   to raise specific antibodies, as assay reagents, as
CC   diagnostic tissue markers, for the isolation of cognate receptors,
CC   ligands and binding proteins, and as biologically active agents.
```

```
CC   Nucleotides encoding the protein may be used as primers and probes or
CC   antisense molecules, and in gene therapy. Cells transformed with these
CC   nucleotides may be used to screen for agonists and antagonists which are
CC   potentially useful therapeutically.
XX
SQ   Sequence 708 BP; 158 A; 195 C; 169 G; 186 T; 0 other;


alignment_scores:
            Quality:  644.00              Length:    234
              Ratio:  3.303                Gaps:      4
 Percent Similarity:  83.333   Percent Identity: 55.556

alignment_block:
 US-09-544-776-2 x Z38318   ..

 Align seg 1/1  to: Z38318  from: 1  to: 708

     142 ArgProProProProProProAlaSerValSerProGlnAlaGluProVa 158
         ||||||      |||   |||:::         |||   :::||||||
      17 CGGCCACTCAGTCCCATTCCATCTCCTCGTCGTCCT...TCGGAGCCG.. 61

     158 lTrpThrProProAlaProAlaProAla..AlaProProSerThrProAl 174
             :::   |||   ||||||   |||  :::|||   :::   |||||
      62 ....AGCCGTCCGCGCCCGGCGGCGGCGGGAGCCCAGGAGCCTGCCCCGC 107

     174 aAlaProLysArgArgGlySerSerGlySerValValValAspLeuLeuT 191
         |         :::      ||||||:::   :::|||   ||||||:::
     108 CCTGGGGACGAAGAGCTGCAGCTCCTCCTGTGCGGTGCACGATCTGATTT 157

     191 yrTrpArgAspIleLysLysThrGlyValValPheGlyAlaSerLeuPhe 207
         ::||||||||||:::|||||||||||   ||||||||:::::::|||:::
     158 TCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCACCACGCTGATC 207

     208 LeuLeuLeuSerLeuThrValPheSerIleValSerValThrAlaTyrIl 224
         :::||||||||||:::::||||||:::::::||||||:::::::|||::
     208 ATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTGGTTTCTTACCT 257

     224 eAlaLeuAlaLeuLeuSerValThrIleSerProArgIleTyrLysGlyV 241
         :   |||||||||||||||||||||||||||   |||||||||||||:::|
     258 CATCCTGGCTCTTCTCTCTGTCACCATCAGCTTCAGGATCTACAAGTCCG 307

     241 alIleGlnAlaIleGlnLysSerAspGluGlyHisProPheArgAlaTyr 257
         ||||||||||:::|||||||||:::|||||||||||||||:::||||||
     308 TCATCCAAGCTGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTAC 357

     258 LeuGluSerGluValAlaIleSerGluGluLeuValGlnLysTyrSerAs 274
         |||:::   :::::::::::|||:::|||      ::::::|||   ||
     358 CTGGACGTAGACATTACTCTGTCCTCAGAAGCTTTCCATAATTACATGAA 407

     274 nSerAlaLeuGlyHisValAsnCysThrIleLysGluLeuArgArgLeuP 291
         |:::|||:::   |||:::|||   :::::::|||   :::   |||||||
     408 TGCTGCCATGGTGCACATCAACAGGGCCCTGAAACTCATTATTCGTCTCT 457

     291 heLeuValAspAspLeuValAspSerLeuLysPheAlaValLeuMetTrp 307
         ||||||||:::|||||||||||||||||||||:::||||||:::||||||
     458 TTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGTCTTCATGTGG 507

     308 ValPheThrTyrValGlyAlaLeuPheAsnGlyLeuThrLeuLeuIleLe 324
         ::::::|||||||||||||||:::|||||||||:::||||||||||||||
     508 CTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCTTCTAATTCT 557

     324 uAlaLeuIleSerLeuPheSerValProValIleTyrGluArgHisGlnA 341
         ||||   :::   :::|||||||||||||:::::::||||||:::::::::
     558 TGCTGAACTGCTCATTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGA 607

     341 laGlnIleAspHisTyrLeuGlyLeuAlaAsnLysAsnValLysAspAla 357
         ::|||||||||||||||:::|||:::|||:::   :::::::|||:::
     608 CCCAGATTGATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATT 657

     358 MetAlaLysIleGlnAlaLysIleProGlyLeu...LysArgLysAlaGl 373
         :::   |||||||||||||||:::||||||:::   |||:::|||||||||
     658 GTTGAAAAGATCCAAGCAAAACTCCCTGGAATCGCCAAAAAAAAGGCAGA 707
```

```
373 u 373
    |
708 A 708
```